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[54] **SUBUNITS OF GLUTAMATE RECEPTORS, THEIR PREPARATION AND THEIR USE**

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[52] **U.S. Cl.** **536/23.1; 536/243; 530/350**

[58] **Field of Search** **536/23.1, 24.3; 530/350; 514/44; 435/69.1, 6**

[56] **References Cited**

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[57] **ABSTRACT**

The invention relates to novel subunits for glutamate receptors and to the DNA sequences coding therefor, and to processes for preparing DNA sequences and receptors. The invention furthermore relates to methods for identifying functional ligands for these receptors.

5 Claims, No Drawings

SUBUNITS OF GLUTAMATE RECEPTORS, THEIR PREPARATION AND THEIR USE

This application is a 371 of PCT/EP95/00290 filed 27 Jan. 95, published as WO95/21188 Aug. 10, 1995. The invention relates to the expression of novel variants of ionotropic glutamate receptor subunits in eukaryotic cells and to methods for finding functional ligands for corresponding glutamate receptor channels.

Glutamate is the most important excitatory neurotransmitter in the central nervous system (TIPS 11, 1990, 126-132; Pharmacological Reviews 40, 1989, 143-210; TIPS 13, 1992, 291-296) and is involved in numerous pathophysiological processes such as epilepsy, schizophrenia, ischemia. Glutamate receptors are therefore potential sites of attack for appropriate drugs.

To date, the primary structure has been elucidated for some subunits of AMPA, kainate and NMDA receptors and some metabotropic receptors (Nature 342, 1989, 643; Science 249, 1990, 556; Neuron 8, 1992, 169; Science 256, 1992, 1217; Nature 358, 1992, 36).

Four AMPA-glutamate receptor subunits of the rat have hitherto been described in the literature, GluRA, GluRB, GluRC and GluRD, each of which occurs in two splicing variants "flip" and "flop" (Science 249, 1990, 1580). In addition, RNA editing which affects the Q/R site of the second transmembrane domain has been shown for mouse and rat GluRB. These two GluRB variants differ considerably in their electrophysiological properties (Cell 67, 1991, 11-19; Neuron 8; 1992, 189-198). The human cDNA for GluRAflip and GluRAflop has likewise been published (PNAS U.S.A. 88, 1991, 7557-7561; PNAS USA 89, 1992, 1443-1447).

We have now found variants of the human glutamate receptor subunits A, B, C and D, as well as DNA sequences which code for such subunits. These subunits lead to GluR channels with specific electrophysiological properties.

We have found that the first amino acid of the flip/flop region of GluRA, GluRB, GluRC and GluRD can be in the form of glycine (G) or arginine (R) due to RNA editing. The names of the corresponding subunits are as follows:
GluRAflipG, GluRAflipR, GluRAflopG, GluRAflopR
GluRBflipQ-G, GluRBflipQ-R, GluRBflopQ-G,
GluRBflopQ-R
GluRBflipR-G, GluRBflipR-R, GluRBflopR-G,
GluRBflopR-R
GluRCflipG, GluRCflipR, GluRCflopG, GluRCflopR
GluRDflipG, GluRDflipR, GluRDflopG, GluRDflopR

In the case of GluRB the RNA editing known for the rat has been taken into account in the naming of the corresponding variants.

Furthermore, a variant of GluRA produced by alternative splicing, in which a 240 bp fragment is missing in the 5' region of the GluRA cDNA and thus the corresponding protein is truncated by 80 amino acids, has been found. The names of the corresponding subunits are as follows:

GluRA~~240~~flipG, GluRA~~240~~flipR,
GluRA~~240~~flopG, GluRA~~240~~flopR

The following DNA and amino-acid sequences all relate to human glutamate receptor subunits.

SEQ ID NO: 1 depicts the cDNA sequence of GluRAflipG and the polypeptide sequence (SEQ ID NO: 2) derived therefrom;

SEQ ID NO: 3 depicts the cDNA sequence of GluRAflopG, and

SEQ ID NO: 4 depicts the polypeptide sequence derived therefrom.

Compared with the GluRAflipG cDNA, the GluRAflipR cDNA has a base exchange at position bp 2269 which converts a glycine codon (GGA) into an arginine codon (AGA). A corresponding statement applies to GluRAflopR.

The GluRA~~240~~ variants correspond to the said GluRA variants but have a deletion: bp 221-460 relative to SEQ ID NO: 1 and 3.

SEQ ID NO: 5 depicts the cDNA sequence of GluRBflipQ-G and the polypeptide sequence derived therefrom (SEQ ID NO: 6); SEQ ID NO: 7 depicts the cDNA sequence of GluRBflopQ-G, and SEQ ID NO: 8 depicts the polypeptide sequence derived therefrom.

Compared with GluRBflipQ-G, the cDNA for GluRBflipQ-R has a base exchange at position bp 2290 which converts a glycine codon (GGA) into an arginine codon (AGA). A corresponding statement applies to GluRBflopQ-R.

Compared with the abovementioned GluRB variants, the cDNA molecules for GluRBflipR-G, GluRBflipR-R, GluRBflopR-G and GluRBflopR-R have a base exchange at position bp 1820 which converts a glutamine codon (CAG) into an arginine codon (CGG).

SEQ ID NO: 9 depicts the cDNA sequence of GluRCflipG and

SEQ ID NO: 10 depicts the polypeptide sequence derived therefrom.

SEQ ID NO: 11 shows the cDNA sequence of GluRCflopG and

SEQ ID NO: 12 depicts the polypeptide sequence derived therefrom.

Compared with GluRCflipG and GluRCflopG, respectively, the cDNA molecules for GluRCflipR and GluRCflopR have a base exchange at position bp 2377 which converts a glycine codon (GGA) into an arginine codon (AGA).

SEQ ID NO: 13 depicts the cDNA sequence of GluRDflipG and

SEQ ID NO: 14 depicts the polypeptide sequence derived therefrom.

SEQ ID NO: 15 shows the cDNA sequence of GluRDflopG and

SEQ ID NO: 16 depicts the polypeptide sequence derived therefrom.

Compared with GluRDflipG and GluRDflopG, respectively, the cDNA molecules for GluRDflipR and GluRDflopR have a base exchange at position bp 2293 which converts a glycine codon (GGA) into an arginine codon (AGA).

Other suitable DNA sequences are those which although they have a different nucleotide sequence from that detailed in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 code for the polypeptide chain detailed in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, or parts thereof as a consequence of the degeneracy of the genetic code. Also suitable are those DNA sequences which code for AMPA-glutamate receptor subunits and which hybridize under standard conditions with the nucleotide sequence depicted in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 or with a nucleotide sequence which codes for the protein depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. Standard conditions mean, for example, temperatures of from 42° to 58° C. in an aqueous buffer solution with a concentration of from 0.1 to 1×SSC (1×SSC: 0.15M NaCl, 15 mM sodium citrate pH 7.2). The experimental conditions for DNA hybridization are described in textbooks of genetic manipulation, for example in Sambrook et al., Molecular Cloning, Cold Spring Harbor Laboratory, 1989.

We have furthermore found genetic engineering processes for preparing these subunits. We have additionally found that the DNA sequences coding for these receptor subunits can be used to find functional ligands for these receptors. The invention furthermore relates to methods for identifying functional ligands for AMPA-glutamate receptors, which comprise transfecting cells with sequences which code for AMPA-GluR subunits, isolating the membranes of these cells, and carrying out conventional receptor-binding experiments with these membranes.

Another method according to the invention for identifying functional ligands for AMPA-glutamate receptors comprises causing in cells which have been transfected with one or more DNA sequences which code for AMPA-GluR subunits an effect on the signal transduction pathway due to binding of the ligands to the receptor, which is detected by a receptor system, for example the intracellular Ca^{++} concentration after ligand binding by fluorimetric methods (Anal. Biochem. 209, 1993, 343).

The novel polypeptides and DNA sequences can be prepared by using conventional methods of genetic engineering. Thus, mRNA can be isolated from brain tissue and converted into double-stranded cDNA. This cDNA can be used as template for the polymerase chain reaction. It is thus possible by using specific primers under suitable reaction conditions to amplify the appropriate cDNA. The use of suitable primers makes it possible to sequence the amplified cDNA without previous cloning. The double-stranded cDNA can also be integrated in λ vectors, eg. λ gt 10 or λ ZAP, in order to generate a brain-specific cDNA bank. A cDNA bank of this type can be screened with radiolabeled DNA or RNA probes in order to identify clones which display homology with the hybridization probe. The methods used for this are described, for example, in Current Protocols in Molecular Biology (edited by F. M. Ausubel et al.) 1989, ISBN 0-471 50338-x (Vol. 1 and 2), for the polymerase chain reaction in Saiki et al., Science, 230 (1985) 1350-54 and Mullis and Faloona, Meth. Enzymol., 155 (1987) 335-350.

The cDNA characterized in this way can easily be obtained using restriction enzymes. The fragments resulting from this can be used, where appropriate in conjunction with chemically synthesized oligonucleotides, adaptors or gene fragments, to clone the sequences coding for the protein. Incorporation of the gene fragments or synthetic DNA sequences into cloning vectors, e.g. the commercial plasmids M13mp18 or Bluescript, is carried out in a conventional way. The genes or gene fragments can also be provided with suitable control regions which have been chemically synthesized or isolated from bacteria, phages, eukaryotic cells or their viruses and which make it possible to express the proteins in various host systems.

The transformation or transfection of suitable host organisms with hybrid plasmids has likewise been described in detail (M. Wigler et al., Cell, 16 (1979), 777-785; F. L. Graham and A. J. van der Eb, Virology, 52 (1973), 456-467).

On expression in mammalian cells it is possible to use vectors which place the gene to be expressed, in this case the cDNA sequences coding for the AMPA-glutamate receptor subunits described herein, under the control of the mouse metallothionein, the viral SV40 or the cytomegalovirus promoter (J. Page Martin, Gene, 37 (1985), 139-144). Needed for expression is the presence of the methionine start codon of the gene which codes for these subunits of AMPA-glutamate receptors. Clones which have copies of these vectors as episomes or integrated into the genome are then

isolated. It is particularly advantageous to integrate the foreign gene into a vector which contains the cytomegalovirus promoter.

As an alternative to this, cells can be transfected with a suitable vector in such a way that the transient expression of the DNA introduced in this way is sufficient for pharmacological characterization of the expressed heterologous polypeptides. In this case too, control of expression by the cytomegalovirus promoter is particularly advantageous.

It is furthermore possible to prepare functional AMPA-glutamate receptors by transfecting one or more different DNA sequences from the group of AMPA-GluR subunits together into cells. AMPA-glutamate receptors with different subunits can be obtained in this way.

The use of shuttle vectors is very suitable in conjunction with prokaryotic sequences which code for replication in bacterial cells and antibiotic resistance. The construction and replication of the plasmid take place initially in bacterial cells; this is followed by transfer into eukaryotic cells, e.g. into the human embryonic kidney cell line HEK 293.

It is also possible to use other cell systems, e.g. yeast and other fungi, insect cells as well as animal and human cells such as CHO, COS and L cells in conjunction with suitable expression vectors for the expression of the cloned cDNA.

The eukaryotic expression systems have the advantage that they are able to express their products efficiently and usually in native form. They have furthermore the ability to carry out post-translational modification of their products.

The expressed receptor proteins can be solubilized by detergents and purified by affinity chromatography by conventional methods. The pure polypeptide can, after crystallization and X-ray structural analysis or other physical methods such as NMR or scanning tunneling microscopy, be used to elucidate first the spatial structure of the receptor and then the spatial structure of the ligand binding site.

The expressed receptor proteins can, after appropriate purification, also be used as antigens for generating polyclonal or monoclonal antibodies. These antibodies in turn can be used where appropriate for diagnostic purposes. Another possible use of such antibodies is as aids to rational drug design. Thus, the receptor-specific antibodies can be employed as antigen for generating anti-idiotypic antibodies. Such antibodies may represent an image of defined regions of the receptor and be used for screening for specific receptor ligands or for rational drug design.

Receptor-expressing cell lines represent an important instrument in screening for specific receptor ligands. The membranes of these cells can be used for a receptor binding assay for this purpose. Information about the mode of action (agonism/antagonism) of a receptor ligand can be obtained by providing cells, which have been transfected with a DNA sequence according to the invention, with a suitable reporter system. Suitable reporter systems are those in which a promoter which is regulated by compounds of the signal transduction pathway (second messenger) is functionally connected to a gene for a product which can easily be detected, such as luciferase. Such reporter systems are disclosed, for example, in Science 252, (1991) 1424, Proc. Natl. Acad. Sci. U.S.A. 88 (1991) 5061 or Journal of Receptor Res. 13, (1993) 79. A suitable promoter which is, for example, regulated by the intracellular Ca^{++} concentration is that of the fos gene. It is also possible to detect changes in the intracellular Ca^{++} concentration directly using fluorescent dyes, eg. FURA 2AM.

Furthermore, the current flowing through the cell membrane as a function of the ligand binding can be measured.

Because of the degeneracy of the genetic code, it is possible to use DNA sequences other than those described

here, e.g. chemically synthesized genes with a different DNA sequence, for the expression of the described subunits of human AMPA-glutamate receptors.

The invention makes it possible to identify and characterize substances which bind to the receptor described herein and there have an agonistic or antagonistic action.

The invention furthermore relates to the use of oligonucleotides which are derived from the structure described in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 as antisense molecules for switching off genes in a targeted manner.

The invention also makes it possible to prepare synthetic oligonucleotides with which the expression of AMPA-glutamate receptor subunits can be specifically inhibited by intracerebroventricular administration, as has been described, for example, for NMDA receptors (Nature 363, 1993, 260).

Other embodiments of the invention are described in detail in the examples.

For genetic engineering methods, reference may be made, for example, to the handbook by Sambrook et al., Molecular Cloning, Cold Spring Harbor Laboratory, 1989, or DNA cloning, Vol. I to III, IRI Press 1985 to 1987, edited by D. M. Glover.

EXAMPLE 1

Isolation of cDNA molecules which code for the human AMPA-glutamate receptor subunits GluRA and GluRA Δ 1240.

The polymerase chain reaction (PCR) technique was used to amplify three cDNA fragments which are specific for the human AMPA-glutamate receptor subunit GluRA from two commercially available human brain cDNA libraries. To increase the specificity of amplification, the 2-stage PCR method described hereinafter was carried out: in each case 10 μ l of lysate from a human temporal cortex cDNA library (titer: 1.5×10^{11} phages/ml; vector lambda ZAP; GluRA cDNA fragment bp 1-839) or a human nucleus accumbens cDNA library (titer: $1-9 \times 10^9$ phages/ml; vector lambda gt10; GluRA cDNA fragments 1-1421 and 1407-2721) were used as templates for the first PCR reaction with the primer oligonucleotides A and B. The volumes of the reaction mixtures were 100 μ l in each case, 20 pmol of each of the various primers were employed, and the reaction buffer contained 10 mM tris-HCl pH 8.5, 50 mM KCl, 1.5 mM MgCl₂, and 0.2 mM each of dATP, dCTP, dGTP and dTTP. 20 cycles with the following temperature profile were carried out: 94° C. for 1 minute, 55° C. for 1 minute, 72° C. for 1 minute. A Perkin-Elmer type 9600 thermocycler was used.

After the PCR had been carried out, in each case 10 μ l of the PCR mixtures were removed and used as templates for a second PCR with primers C and D. The reaction and buffer conditions were the same as for the first PCR, but the number of cycles was increased to 35. The amplified cDNA fragments were cloned into the vector pCRII in accordance with the manufacturer's instructions using the Invitrogen TA cloning kit.

The primer oligonucleotides for amplification of the human GluRA cDNA fragment which comprises base pairs 1-1431 had the following sequences:

Primer A: 5'-ATCTATGATTGGACCTGGGC-3' (SEQ ID NO: 17)

Primer B: 5'-ACATCTGCTCTTCCATAGACCAGC-3' (SEQ ID NO: 18)

Primer C: 5'-TGCGATAAGCTTATGCAGCACATTTTGCCTTCTTCTGC-3' (SEQ ID NO: 19)

Primer D: 5'-ATGCCATTCCAGGCCTTCGTGTCA-3' (SEQ ID NO: 20)

The primer oligonucleotides for amplification of the human GluRA cDNA fragment which comprises base pairs 1407-2721 had the following sequences:

Primer A: 5'-GATGGAAAATACGGAGCCCGA-3' (SEQ ID NO: 21)

Primer B: 5'-GCTGGGGAGCCGAGCCTGCTC-3' (SEQ ID NO: 22)

Primer C: 5'-TGACACGAAGGCCTGGAATGGCAT-3' (SEQ ID NO: 23)

Primer D: 5'-TGCGATGAATTCTTACAATCCCGTGGCTCCCAAGGGCAT-3' (SEQ ID NO: 24)

The primer oligonucleotides for amplification of the human GluRA cDNA fragment which comprises base pairs 1-839 had the following sequences:

Primer A: SEQ ID NO: 17

Primer B: 5'-TACTTGGGTCTCTTCCAGTCCA-3' (SEQ ID NO: 25)

Primer C: SEQ ID NO: 20

Primer D: 5'-TGTGTGGTCTCGAGCATCACTATT-3' (SEQ ID NO: 26)

Standard methods of genetic engineering (see, for example, Sambrook et al. (1989), Molecular Cloning, Cold Spring Harbor Laboratory) were used to assemble the amplified cDNA fragments in each case to the complete coding regions of GluRA and GluRA Δ 1240.

EXAMPLE 2

Isolation of cDNA molecules for human glutamate receptor subunits A, B, C and D

cDNA fragments which are specific for human glutamate receptor subunits A, B, C and D were obtained by screening the following commercially available human brain cDNA libraries:

Hippocampus (from Stratagene)

Cerebellum (from Clontech and Stratagene)

Nucleus accumbens (Clontech)

The screening probes used were PCR fragments 600-3000 bp in size which had been amplified from the cDNA molecules for rat GluRA, B, C and D which had been cloned in pBluescript. In each case 1 ng of plasmid DNA was employed as template. The primer concentrations and buffer conditions for the PCRs corresponded to those in Example 1 but in each case 2 μ l of the dNTP labeling mixture from the Boehringer Mannheim DNA labeling and detection kit were employed as nucleotide source. 35 cycles with the following temperature profile were carried out: 94° C. for 2 minutes, 55° C. for 2 minutes, 72° C. for 3 minutes. The Dig-dUTP-labeled fragments were purified on a Sea-plaque agarose gel. The screening procedure was carried out in accordance with the instructions in the manual for the abovementioned kit. The GluR cDNA fragments of the lambda clones derived from the screening were cloned by conventional methods of genetic engineering into the vector pBluescript and assembled to give the complete cDNA molecules of the various GluR variants.

EXAMPLE 3

Transient expression of the cloned human GluR genes in HEK293 cells.

Unless stated otherwise, the cell culture was carried out as described by Lindl and Bauer, Zell-und Gewebekultur, Gustav Fischer Verlag.

The GluR cDNA molecules from Examples 1 and 2 were cloned into conventional plasmids such as pBluescript (from

Stratagene) and PCRII (from Invitrogen) during their isolation. The cloned GluR fragments in each case comprise the entire open reading frame including start and stop codons and at least 40 bp of the 5' non-translated region preceding the start codon.

For the transient expression in eukaryotic cell lines, the cloned GluR fragments were cloned into the expression vector pcDNA3 (from Invitrogen). The recombinant plasmids resulting therefrom were replicated in a known manner.

HEK 293 cells were cultivated under standard conditions. After trypsinization, the cells were taken up in DMEM (Gibco) which contained 3.7 g/l NaHCO₃, and 10 cm Petri dishes were inoculated with 1.5×10⁶ cells. These cells were then cultivated at 37° C. and 5% CO₂ for 24 h.

The DNA to be transfected was prepared as follows: 20 µg of the DNA solution (1 mg/ml), purified using the Quiagen® system from Diagen, were mixed with 437 µl of H₂O, and then 62.5 µl of 2M CaCl₂, and finally 500 µl of PBS, were added. Ca⁺⁺ precipitates formed within 10 min at room temperature.

The solution was placed on a 10 cm culture dish containing the HEK 293 cells cultivated by the above method. After cautious mixing, the cells were cultivated in an incubator at 37° C./3% CO₂ for 15 to 20 h. Then 5 ml of serum-free medium were cautiously added. After removal of all the medium and repetition of the washing process with 5 ml of medium, 10 ml of medium were added to the cells. After incubation at 37° C. and 5% CO₂ for 48 h, the cells were suitable for pharmacological and electrophysiological investigations.

Alternatively, the DNA was also introduced into the cells with liposome mediation. Lipofectin from GIBCO-BRL was employed for this in accordance with the manufacturer's instructions.

EXAMPLE 4

Expression of the AMPA-glutamate receptor subunits in oocytes

To prepare cRNA, the corresponding cDNA molecules which code for the glutamate receptor subunits were cloned by standard protocols into the Bluescript plasmid (Stratagene) which had been cleaved with EcoRI.

Plasmid DNA was obtained by standard methods after growing of the Bluescript clones which code for subunits of

AMPA-glutamate receptors. This plasmid DNA was cleaved with the restriction enzyme Not I and employed for the in vitro transcription. The transcription was started from the T3 or T7 promoter and carried out under standard conditions in accordance with the Stratagene in vitro transcription kit.

For the expression of the receptor subunits, in each case 10 ng of cRNA were injected either alone or combined with other cRNA into oocytes which had been explanted from the clawed frog *Xenopus laevis* [C. Methfessel et al., Pflügers Arch. 407, 577, (1986)]. The oocytes were incubated in OR-2 (92.5 mM NaCl, 2.5 mM KCl, 1 mM Na₂HPO₄, 5 mM HEPES, 1 mM MgCl₂, 1 mM CaCl₂, 0.5 g/l polyvinylpyrrolidone, pH 7.2 with the addition of 4 µg/ml Zinacef and 100 U/ml Penstrep) at 19° C. 24 hours after the injection, the oocytes were treated with collagenase (Sigma Type II) (1 mg/ml in OR-2 for 1 hour). Electrophysiological recordings were made 2–6 days after injection of the cRNA. A 2-electrode voltage clamp configuration was used for this with a TEC 01C amplifier (NPI Electronic, Tamm, Germany). During the electrophysiological measurements, the oocytes were perfused with normal frog Ringer solution (NRF: 115 mM NaCl, 2.5 mM KCl, 1.8 mM CaCl₂, 10 mM HEPES, pH 7.2).

EXAMPLE 5

Stable expression of the glutamate receptor subunits in HEK 293 cells

The glutamate receptor cDNA molecules described in Examples 1 and 2 were cloned into the eukaryotic expression vectors pcDNA3 and pRc/CMV (from Invitrogen). These expression constructs were introduced singly or in combination into HEK 293 cells by electroporation by the following protocol: HEK 293 cells (ATCC) were cultivated in RPMI 1640 medium (Glutamax I from Gibco BRL) containing 10% FCS (Gibco BRL) under 5% CO₂. For the electroporation, 10⁷ cells were transfected in 0.8 ml of PBS with 20 µg of the expression construct using an electroporator (BTX, electro cell manipulator 600, 3 µF, 130 V, 72 ohm). The cells were subsequently incubated in culture medium for 24 h and then transferred into selection medium (RPMI medium with 600 µg/ml G418 sulfate, geneticin). Stable geneticin-resistant cell clones were isolated after 10–12 days by plating out and were expanded and analyzed by a membrane binding assay.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i i i) NUMBER OF SEQUENCES: 26

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA to mRNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) DEVELOPMENTAL STAGE: Adult
- (C) TISSUE TYPE: Brain

-continued

(i x) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 144..2861

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GAAAGGAAGG AAGCAAGCAA GCAAGGAAGG AACTGCAGGA GGAAAAGAAC AGGCAGAACA      60
GCGAAAAGAA TAAAGGGAAA GGGGGGGAAA CACCAAATCT ATGATTGGAC CTGGGCTTCT      120
TTTTCGCCAA TGCAAAAAGG AAT ATG CAG CAC ATT TTT GCC TTC TTC TGC      170
                        Met Gln His Ile Phe Ala Phe Phe Cys
                          1                      5

ACC GGT TTC CTA GGC GCG GTA GTA GGT GCC AAT TTC CCC AAC AAT ATC      218
Thr Gly Phe Leu Gly Ala Val Val Gly Ala Asn Phe Pro Asn Asn Ile
 10                    15                20                25

CAG ATC GGG GGA TTA TTT CCA AAC CAG CAG TCA CAG GAA CAT GCT GCT      266
Gln Ile Gly Gly Leu Phe Pro Asn Gln Gln Ser Gln Glu His Ala Ala
                    30                    35                    40

TTT AGA TTT GCT TTG TCG CAA CTC ACA GAG CCC CCG AAG CTG CTC CCC      314
Phe Arg Phe Ala Leu Ser Gln Leu Thr Glu Pro Pro Lys Leu Leu Pro
                    45                    50                    55

CAG ATT GAT ATT GTG AAC ATC AGC GAC AGC TTT GAG ATG ACC TAT AGA      362
Gln Ile Asp Ile Val Asn Ile Ser Asp Ser Phe Glu Met Thr Tyr Arg
                    60                    65                    70

TTC TGT TCC CAG TTC TCC AAA GGA GTC TAT GCC ATC TTT GGG TTT TAT      410
Phe Cys Ser Gln Phe Ser Lys Gly Val Tyr Ala Ile Phe Gly Phe Tyr
                    75                    80                    85

GAA CGT AGG ACT GTC AAC ATG CTG ACC TCC TTT TGT GGG GCC CTC CAC      458
Glu Arg Arg Thr Val Asn Met Leu Thr Ser Phe Cys Gly Ala Leu His
 90                    95                    100                105

GTC TGC TTC ATT ACG CCG AGC TTT CCC GTT GAT ACA TCC AAT CAG TTT      506
Val Cys Phe Ile Thr Pro Ser Phe Pro Val Asp Thr Ser Asn Gln Phe
                    110                115

GTC CTT CAG CTG CGC CCT GAA CTG CAG GAT GCC CTC ATC AGC ATC ATT      554
Val Leu Gln Leu Arg Pro Glu Leu Gln Asp Ala Leu Ile Ser Ile Ile
                    125                130                135

GAC CAT TAC AAG TGG CAG AAA TTT GTC TAC ATT TAT GAT GCC GAC CGG      602
Asp His Tyr Lys Trp Gln Lys Phe Val Tyr Ile Tyr Asp Ala Asp Arg
                    140                145                150

GGC TTA TCC GTC CTG CAG AAA GTC CTG GAT ACA GCT GCT GAG AAG AAC      650
Gly Leu Ser Val Leu Gln Lys Val Leu Asp Thr Ala Ala Glu Lys Asn
                    155                160                165

TGG CAG GTG ACA GCA GTC AAC ATC TTG ACA ACC ACA GAG GAG GGA TAC      698
Trp Gln Val Thr Ala Val Asn Ile Leu Thr Thr Thr Glu Glu Gly Tyr
170                    175                180                185

CGG ATG CTC TTT CAG GAC CTG GAG AAG AAA AAG GAG CGG CTG GTG GTG      746
Arg Met Leu Phe Gln Asp Leu Glu Lys Lys Lys Glu Arg Leu Val Val
                    190                195                200

GTG GAC TGT GAA TCA GAA CGC CTC AAT GCT ATC TTG GGC CAG ATT ATA      794
Val Asp Cys Glu Ser Glu Arg Leu Asn Ala Ile Leu Gly Gln Ile Ile
                    205                210                215

AAG CTA GAG AAG AAT GGC ATC GGC TAC CAC TAC AIT CTT GCA AAT CTG      842
Lys Leu Glu Lys Asn Gly Ile Gly Tyr His Tyr Ile Leu Ala Asn Leu
                    220                225                230

GGC TTC ATG GAC ATT GAC TTA AAC AAA TTC AAG GAG AGT GGC GCC AAT      890
Gly Phe Met Asp Ile Asp Leu Asn Lys Phe Lys Glu Ser Gly Ala Asn
                    235                240                245

GTG ACA GGT TTC CAG CTG GTG AAC TAC ACA GAC ACT ATT CCG GCC AAG      938
Val Thr Gly Phe Gln Leu Val Asn Tyr Thr Asp Thr Ile Pro Ala Lys
250                    255                260                265

ATC ATG CAG CAG TGG AAG AAT AGT GAT GCT CGA GAC CAC ACA CGG GTG      986

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-continued

Ile	Met	Gln	Gln	Trp	Lys	Asn	Ser	Asp	Ala	Arg	Asp	His	Thr	Arg	Val	
				270					275					280		
GAC	TGG	AAG	AGA	CCC	AAG	TAC	ACC	TCT	GCG	CTC	ACC	TAC	GAT	GGG	GTG	1034
Asp	Trp	Lys	Arg	Pro	Lys	Tyr	Thr	Ser	Ala	Leu	Thr	Tyr	Asp	Gly	Val	
			285					290					295			
AAG	GTG	ATG	GCT	GAG	GCT	TTC	CAG	AGC	CTG	CGG	AGG	CAG	AGA	ATT	GAT	1082
Lys	Val	Met	Ala	Glu	Ala	Phe	Gln	Ser	Leu	Arg	Arg	Gln	Arg	Ile	Asp	
		300					305					310				
ATA	TCT	CGC	CGG	GGG	AAT	GCT	GGG	GAT	TGT	CTG	GCT	AAC	CCA	GCT	GTT	1130
Ile	Ser	Arg	Arg	Gly	Asn	Ala	Gly	Asp	Cys	Leu	Ala	Asn	Pro	Ala	Val	
	315					320					325					
CCC	TGG	GGC	CAA	GGG	ATC	GAC	ATC	CAG	AGA	GCT	CTG	CAG	CAG	GTG	CGA	1178
Pro	Trp	Gly	Gln	Gly	Ile	Asp	Ile	Gln	Arg	Ala	Leu	Gln	Gln	Val	Arg	
330					335					340					345	
TTT	GAA	GGT	TTA	ACA	GGA	AAC	GTG	CAG	TTT	AAT	GAG	AAA	GGA	CGC	CGG	1226
Phe	Glu	Gly	Leu	Thr	Gly	Asn	Val	Gln	Phe	Asn	Glu	Lys	Gly	Arg	Arg	
				350					355					360		
ACC	AAC	TAC	ACG	CTC	CAC	GTG	ATT	GAA	ATG	AAA	CAT	GAC	AGC	ATC	CGA	1274
Thr	Asn	Tyr	Thr	Leu	His	Val	Ile	Glu	Met	Lys	His	Asp	Ser	Ile	Arg	
			365					370					375			
AAG	ATT	GGT	TAC	TGG	AAT	GAA	GAT	GAT	AAG	TTT	GTC	CCT	GCA	GCC	ACC	1322
Lys	Ile	Gly	Tyr	Trp	Asn	Glu	Asp	Asp	Lys	Phe	Val	Pro	Ala	Ala	Thr	
		380					385					390				
GAT	GCC	CAA	GCT	GGG	GGC	GAT	AAT	TCA	AGT	GTT	CAG	AAC	AGA	ACA	TAC	1370
Asp	Ala	Gln	Ala	Gly	Gly	Asp	Asn	Ser	Ser	Val	Gln	Asn	Arg	Thr	Tyr	
	395					400					405					
ATC	GTC	ACA	ACA	ATC	CTA	GAA	GAT	CCT	TAT	GTG	ATG	CTC	AAG	AAG	AAC	1418
Ile	Val	Thr	Thr	Ile	Leu	Glu	Asp	Pro	Tyr	Val	Met	Leu	Lys	Lys	Asn	
410					415					420					425	
GCC	AAT	CAG	TTT	GAG	GGC	AAT	GAC	CGT	TAC	GAG	GGC	TAC	TGT	GTA	GAG	1466
Ala	Asn	Gln	Phe	Glu	Gly	Asn	Asp	Arg	Tyr	Glu	Gly	Tyr	Cys	Val	Glu	
				430					435					440		
CTG	GCG	GCA	GAG	ATT	GCC	AAG	CAC	GTG	GGC	TAC	TCC	TAC	CGT	CTG	GAG	1514
Leu	Ala	Ala	Glu	Ile	Ala	Lys	His	Val	Gly	Tyr	Ser	Tyr	Arg	Leu	Glu	
			445					450					455			
ATT	GTC	AGT	GAT	GGA	AAA	TAC	GGA	GCC	CGA	GAC	CCT	GAC	ACG	AAG	GCC	1562
Ile	Val	Ser	Asp	Gly	Lys	Tyr	Gly	Ala	Arg	Asp	Pro	Asp	Thr	Lys	Ala	
		460					465						470			
TGG	AAT	GGC	ATG	GTG	GGA	GAG	CTG	GTC	TAT	GGA	AGA	GCA	GAT	GTG	GCT	1610
Trp	Asn	Gly	Met	Val	Gly	Glu	Leu	Val	Tyr	Gly	Arg	Ala	Asp	Val	Ala	
	475					480					485					
GTG	GCT	CCC	TTA	ACT	ATC	ACT	TTG	GTC	CGG	GAA	GAA	GTT	ATA	GAT	TTC	1658
Val	Ala	Pro	Leu	Thr	Ile	Thr	Leu	Val	Arg	Glu	Glu	Val	Ile	Asp	Phe	
490					495					500					505	
TCC	AAA	CCA	TTT	ATG	AGT	TTG	GGG	ATC	TCC	ATC	ATG	ATT	AAA	AAA	CCA	1706
Ser	Lys	Pro	Phe	Met	Ser	Leu	Gly	Ile	Ser	Ile	Met	Ile	Lys	Lys	Pro	
				510					515					520		
CAG	AAA	TCC	AAG	CCG	GGT	GTC	TTC	TCC	TTC	CTT	GAT	CCT	TTG	GCT	TAT	1754
Gln	Lys	Ser	Lys	Pro	Gly	Val	Phe	Ser	Phe	Leu	Asp	Pro	Leu	Ala	Tyr	
			525					530					535			
GAG	ATT	TGG	ATG	TGC	ATT	GTT	TTT	GCC	TAC	ATT	GGA	GTG	AGT	GTT	GTC	1802
Glu	Ile	Trp	Met	Cys	Ile	Val	Phe	Ala	Tyr	Ile	Gly	Val	Ser	Val	Val	
		540				545						550				
CTC	TTC	CTG	GTC	AGC	CGC	TTC	AGT	CCC	TAT	GAA	TGG	CAC	AGT	GAA	GAG	1850
Leu	Phe	Leu	Val	Ser	Arg	Phe	Ser	Pro	Tyr	Glu	Trp	His	Ser	Glu	Glu	
	555					560					565					
TTT	GAG	GAA	GGA	CGG	GAC	CAG	ACA	ACC	AGT	GAC	CAG	TCC	AAT	GAG	TTT	1898
Phe	Glu	Glu	Gly	Arg	Asp	Gln	Thr	Thr	Ser	Asp	Gln	Ser	Asn	Glu	Phe	
570					575					580					585	
GGG	ATA	TTC	AAC	AGT	TTG	TGG	TTC	TCC	CTG	GGA	GCC	TTC	ATG	CAG	CAA	1946

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Gly	Ile	Phe	Asn	Ser	Leu	Trp	Phe	Ser	Leu	Gly	Ala	Phe	Met	Gln	Gln		
				590					595					600			
GGA Gly	TGT Cys	GAC Asp	ATT Ile 605	TCT Ser	CCC Pro	AGG Arg	TCC Ser	CTG Leu	TCT Ser	GGT Gly	CGC Arg	ATC Ile	GTT Val 615	GGT Gly	GGC Gly	1994	
GTC Val	TGG Trp	TGG Trp 620	TTC Phe	TTC Phe	ACC Thr	TTA Leu	ATC Ile 625	ATC Ile	ATC Ile	TCC Ser	TCA Ser	TAT Tyr 630	ACA Thr	GCC Ala	AAT Asn	2042	
CTG Leu	GCC Ala 635	GCC Ala	TTC Phe	CTG Leu	ACC Thr	GTG Val 640	GAG Glu	AGG Arg	ATG Met	GTG Val	TCT Ser 645	CCC Pro	ATT Ile	GAG Glu	AGT Ser	2090	
GCA Ala 650	GAG Glu	GAC Asp	CTA Leu	GCG Ala	AAG Lys 655	CAG Gln	ACA Thr	GAA Glu	ATT Ile 660	GCC Ala	TAC Tyr	GGG Gly	ACG Thr	CTG Leu	GAA Glu 665	2138	
GCA Ala	GGA Gly	TCT Ser	ACT Thr	AAG Lys 670	GAG Glu	TTC Phe	TTC Phe	AGG Arg	AGG Arg 675	TCT Ser	AAA Lys	ATT Ile	GCT Ala	GTG Val 680	TTT Phe	2186	
GAG Glu	AAG Lys	ATG Met	TGG Trp 685	ACA Thr	TAC Tyr	ATG Met	AAG Lys	TCA Ser 690	GCA Ala	GAG Glu	CCA Pro	TCA Ser	GTT Val 695	TTT Phe	GTG Val	2234	
CGG Arg	ACC Thr	ACA Thr 700	GAG Glu	GAG Glu	GGG Gly	ATG Met 705	ATT Ile	CGA Arg	GTG Val	AGG Arg	AAA Lys 710	TCC Ser	AAA Lys	GGC Gly	AAA Lys	2282	
TAT Tyr	GCC Ala 715	TAC Tyr	CTC Leu	CTG Leu	GAG Glu	TCC Ser 720	ACC Thr	ATG Met	AAT Asn	GAG Glu	TAC Tyr 725	ATT Ile	GAG Glu	CAG Gln	CGG Arg	2330	
AAA Lys 730	CCC Pro	TGT Cys	GAC Asp	ACC Thr	ATG Met 735	AAG Lys	GTG Val	GGA Gly	GGT Gly 740	AAC Asn	TTG Leu	GAT Asp	TCC Ser	AAA Lys	GGC Gly 745	2378	
TAT Tyr	GGC Gly	ATT Ile	GCA Ala	ACA Thr 750	CCC Pro	AAG Lys	GGG Gly	TCT Ser	GCC Ala 755	CTG Leu	GGA Gly	GGT Gly	CCC Pro	GTA Val 760	AAC Asn	2426	
CTA Leu	GCG Ala	GTT Val	TTG Leu 765	AAA Lys	CTC Leu	AGT Ser	GAG Glu	CAA Gln 770	GGC Gly	GTC Val	TTA Leu	GAC Asp	AAG Lys 775	CTG Leu	AAA Lys	2474	
AGC Ser	AAA Lys	TGG Trp 780	TGG Trp	TAC Tyr	GAT Asp	AAA Lys	GGG Gly 785	GAA Glu	TGT Cys	GGA Gly	AGC Ser	AAG Lys 790	GAC Asp	TCC Ser	GGA Gly	2522	
AGT Ser	AAG Lys 795	GAC Asp	AAG Lys	ACA Thr	AGC Ser	GCT Ala 800	CTG Leu	AGC Ser	CTC Leu	AGC Ser	AAT Asn 805	GTG Val	GCA Ala	GGC Gly	GTG Val	2570	
TTC Phe 810	TAC Tyr	ATC Ile	CTG Leu	ATC Ile	GGA Gly 815	GGA Gly	CTT Leu	GGA Gly	CTA Leu	GCC Ala 820	ATG Met	CTG Leu	GTT Val	GCC Ala	TTA Leu 825	2618	
ATC Ile	GAG Glu	TTC Phe	TGC Cys	TAC Tyr 830	AAA Lys	TCC Ser	CGT Arg	AGT Ser	GAA Glu 835	TCC Ser	AAG Lys	CGG Arg	ATG Met 840	AAG Lys	GGT Gly	2666	
TTT Phe	TGT Cys	TTG Leu	ATC Ile 845	CCA Pro	CAG Gln	CAA Gln	TCC Ser	ATC Ile 850	AAC Asn	GAA Glu	GCC Ala	ATA Ile	CGG Arg 855	ACA Thr	TCG Ser	2714	
ACC Thr	CTC Leu	CCC Pro 860	CGC Arg	AAC Asn	AGC Ser	GGG Gly	GCA Ala 865	GGA Gly	GCC Ala	AGC Ser	AGC Ser	GGC Gly 870	GGC Gly	AGT Ser	GGA Gly	2762	
GAG Glu	AAT Asn 875	GGT Gly	CGG Arg	GTG Val	GTC Val	AGC Ser 880	CAT His	GAC Asp	TTC Phe	CCC Pro	AAG Lys 885	TCC Ser	ATG Met	CAA Gln	TCG Ser	2810	
ATT Ile 890	CCT Pro	TGC Cys	ATG Met	AGC Ser	CAC His 895	AGT Ser	TCA Ser	GGG Gly	ATG Met	CCC Pro 900	TTG Leu	GGA Gly	GCC Ala	ACG Thr	GGA Gly 905	2858	
TTG	TA	ACT	TGG	GAG	AG	ATG	GG	GAG	AC	GC	AG	GCT	CG	CT	CCC	AG	2911

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340				345				350							
Val	Gln	Phe	Asn	Glu	Lys	Gly	Arg	Arg	Thr	Asn	Tyr	Thr	Leu	His	Val
		355					360					365			
Ile	Glu	Met	Lys	His	Asp	Ser	Ile	Arg	Lys	Ile	Gly	Tyr	Trp	Asn	Glu
	370					375					380				
Asp	Asp	Lys	Phe	Val	Pro	Ala	Ala	Thr	Asp	Ala	Gln	Ala	Gly	Gly	Asp
385					390					395					400
Asn	Ser	Ser	Val	Gln	Asn	Arg	Thr	Tyr	Ile	Val	Thr	Thr	Ile	Leu	Glu
				405					410					415	
Asp	Pro	Tyr	Val	Met	Leu	Lys	Lys	Asn	Ala	Asn	Gln	Phe	Glu	Gly	Asn
			420					425					430		
Asp	Arg	Tyr	Glu	Gly	Tyr	Cys	Val	Glu	Leu	Ala	Ala	Glu	Ile	Ala	Lys
		435					440					445			
His	Val	Gly	Tyr	Ser	Tyr	Arg	Leu	Glu	Ile	Val	Ser	Asp	Gly	Lys	Tyr
	450					455					460				
Gly	Ala	Arg	Asp	Pro	Asp	Thr	Lys	Ala	Trp	Asn	Gly	Met	Val	Gly	Glu
465					470					475					480
Leu	Val	Tyr	Gly	Arg	Ala	Asp	Val	Ala	Val	Ala	Pro	Leu	Thr	Ile	Thr
				485					490					495	
Leu	Val	Arg	Glu	Glu	Val	Ile	Asp	Phe	Ser	Lys	Pro	Phe	Met	Ser	Leu
			500					505					510		
Gly	Ile	Ser	Ile	Met	Ile	Lys	Lys	Pro	Gln	Lys	Ser	Lys	Pro	Gly	Val
		515					520					525			
Phe	Ser	Phe	Leu	Asp	Pro	Leu	Ala	Tyr	Glu	Ile	Trp	Met	Cys	Ile	Val
	530					535					540				
Phe	Ala	Tyr	Ile	Gly	Val	Ser	Val	Val	Leu	Phe	Leu	Val	Ser	Arg	Phe
545					550					555					560
Ser	Pro	Tyr	Glu	Trp	His	Ser	Glu	Glu	Phe	Glu	Glu	Gly	Arg	Asp	Gln
				565					570					575	
Thr	Thr	Ser	Asp	Gln	Ser	Asn	Glu	Phe	Gly	Ile	Phe	Asn	Ser	Leu	Trp
			580					585					590		
Phe	Ser	Leu	Gly	Ala	Phe	Met	Gln	Gln	Gly	Cys	Asp	Ile	Ser	Pro	Arg
		595					600					605			
Ser	Leu	Ser	Gly	Arg	Ile	Val	Gly	Gly	Val	Trp	Trp	Phe	Phe	Thr	Leu
	610					615					620				
Ile	Ile	Ile	Ser	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Thr	Val
625					630					635					640
Glu	Arg	Met	Val	Ser	Pro	Ile	Glu	Ser	Ala	Glu	Asp	Leu	Ala	Lys	Gln
				645					650					655	
Thr	Glu	Ile	Ala	Tyr	Gly	Thr	Leu	Glu	Ala	Gly	Ser	Thr	Lys	Glu	Phe
			660					665					670		
Phe	Arg	Arg	Ser	Lys	Ile	Ala	Val	Phe	Glu	Lys	Met	Trp	Thr	Tyr	Met
		675					680					685			
Lys	Ser	Ala	Glu	Pro	Ser	Val	Phe	Val	Arg	Thr	Thr	Glu	Glu	Gly	Met
	690					695					700				
Ile	Arg	Val	Arg	Lys	Ser	Lys	Gly	Lys	Tyr	Ala	Tyr	Leu	Leu	Glu	Ser
705					710					715					720
Thr	Met	Asn	Glu	Tyr	Ile	Glu	Gln	Arg	Lys	Pro	Cys	Asp	Thr	Met	Lys
				725					730					735	
Val	Gly	Gly	Asn	Leu	Asp	Ser	Lys	Gly	Tyr	Gly	Ile	Ala	Thr	Pro	Lys
			740					745					750		
Gly	Ser	Ala	Leu	Gly	Gly	Pro	Val	Asn	Leu	Ala	Val	Leu	Lys	Leu	Ser
		755					760					765			

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GTC Val	TGC Cys	TTC Phe	ATT Ile	ACG Thr 110	CCG Pro	AGC Ser	TTT Phe	CCC Pro	GTT Val 115	GAT Asp	ACA Thr	TCC Ser	AAT Asn	CAG Gln 120	TTT Phe	506
GTC Val	CTT Leu	CAG Gln	CTG Leu 125	CGC Arg	CCT Pro	GAA Glu	CTG Leu	CAG Gln 130	GAT Asp	GCC Ala	CTC Leu	ATC Ile	AGC Ser 135	ATC Ile	ATT Ile	554
GAC Asp	CAT His	TAC Tyr 140	AAG Lys	TGG Trp	CAG Gln	AAA Lys	TTT Phe 145	GTC Val	TAC Tyr	ATT Ile	TAT Tyr	GAT Asp 150	GCC Ala	GAC Asp	CGG Arg	602
GGC Gly 155	TTA Leu	TCC Ser	GTC Val	CTG Leu	CAG Gln	AAA Lys 160	GTC Val	CTG Leu	GAT Asp	ACA Thr	GCT Ala 165	GCT Ala	GAG Glu	AAG Lys	AAC Asn	650
TGG Trp 170	CAG Gln	GTG Val	ACA Thr	GCA Ala	GTC Val 175	AAC Asn	ATC Ile	TTG Leu	ACA Thr	ACC Thr 180	ACA Thr	GAG Glu	GAG Glu	GGA Gly	TAC Tyr 185	698
CGG Arg	ATG Met	CTC Leu	TTT Phe	CAG Gln 190	GAC Asp	CTG Leu	GAG Glu	AAG Lys 195	AAA Lys	AAG Lys	GAG Glu	CGG Arg	CTG Leu	GTG Val 200	GTG Val	746
GTG Val	GAC Asp	TGT Cys	GAA Glu 205	TCA Ser	GAA Glu	CGC Arg	CTC Leu	AAT Asn 210	GCT Ala	ATC Ile	TTG Leu	GGC Gly	CAG Gln 215	ATT Ile	ATA Ile	794
AAG Lys	CTA Leu	GAG Glu 220	AAG Lys	AAT Asn	GGC Gly	ATC Ile	GGC Gly 225	TAC Tyr	CAC His	TAC Tyr	ATT Ile	CTT Leu 230	GCA Ala	AAT Asn	CTG Leu	842
GGC Gly 235	TTC Phe	ATG Met	GAC Asp	ATT Ile	GAC Asp	TTA Leu 240	AAC Asn	AAA Lys	TTC Phe	AAG Lys	GAG Glu 245	AGT Ser	GGC Gly	GCC Ala	AAT Asn	890
GTG Val 250	ACA Thr	GGT Gly	TTC Phe	CAG Gln 255	CTG Leu	GTG Val	AAC Asn	TAC Tyr	ACA Thr	GAC Asp 260	ACT Thr	ATT Ile	CCG Pro	GCC Ala	AAG Lys 265	938
ATC Ile	ATG Met	CAG Gln	CAG Gln 270	TGG Trp	AAG Lys	AAT Asn	AGT Ser	GAT Asp	GCT Ala 275	CGA Arg	GAC Asp	CAC His	ACA Thr	CGG Arg 280	GTG Val	986
GAC Asp	TGG Trp	AAG Lys	AGA Arg 285	CCC Pro	AAG Lys	TAC Tyr	ACC Thr	TCT Ser 290	GCG Ala	CTC Leu	ACC Thr	TAC Tyr	GAT Asp 295	GGG Gly	GTG Val	1034
AAG Lys	GTG Val 300	ATG Met	GCT Ala	GAG Glu	GCT Ala	TTC Phe	CAG Gln 305	AGC Ser	CTG Leu	CGG Arg	AGG Arg	CAG Gln 310	AGA Arg	ATT Ile	GAT Asp	1082
ATA Ile	TCT Ser 315	CGC Arg	CGG Arg	GGG Gly	AAT Asn	GCT Ala 320	GGG Gly	GAT Asp	TGT Cys	CTG Leu	GCT Ala 325	AAC Asn	CCA Pro	GCT Ala	GTT Val	1130
CCC Pro 330	TGG Trp	GGC Gly	CAA Gln	GGG Gly 335	ATC Ile	GAC Asp	ATC Ile	CAG Gln	AGA Arg	GCT Ala 340	CTG Leu	CAG Gln	CAG Gln	GTG Val	CGA Arg 345	1178
TTT Phe	GAA Glu	GGT Gly	TTA Leu 350	ACA Thr	GGA Gly	AAC Asn	GTG Val	CAG Gln 355	TTT Phe	AAT Asn	GAG Glu	AAA Lys	GGA Gly 360	CGC Arg	CGG Arg	1226
ACC Thr	AAC Asn	TAC Tyr 365	ACG Thr	CTC Leu	CAC His	GTG Val	ATT Ile	GAA Glu 370	ATG Met	AAA Lys	CAT His	GAC Asp 375	AGC Ser	ATC Ile	CGA Arg	1274
AAG Lys	ATT Ile	GGT Gly 380	TAC Tyr	TGG Trp	AAT Asn	GAA Glu	GAT Asp 385	GAT Asp	AAG Lys	TTT Phe	GTC Val	CCT Pro 390	GCA Ala	GCC Ala	ACC Thr	1322
GAT Asp 395	GCC Ala	CAA Gln	GCT Ala	GGG Gly	GGC Gly	GAT Asp 400	AAT Asn	TCA Ser	AGT Ser	GTT Val	CAG Gln 405	AAC Asn	AGA Arg	ACA Thr	TAC Tyr	1370
ATC Ile 410	GTC Val	ACA Thr	ACA Thr	ATC Ile	CTA Leu 415	GAA Glu	GAT Asp	CCT Pro	TAT Tyr	GTG Val 420	ATG Met	CTC Leu	AAG Lys	AAG Lys	AAC Asn 425	1418

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GCC Ala	AAT Asn	CAG Gln	TTT Phe	GAG Glu 430	GGC Gly	AAT Asn	GAC Asp	CGT Arg	TAC Tyr 435	GAG Glu	GGC Gly	TAC Tyr	TGT Cys	GTA Val 440	GAG Glu	1466
CTG Leu	GCG Ala	GCA Ala	GAG Glu 445	ATT Ile	GCC Ala	AAG Lys	CAC His	GTG Val 450	GGC Gly	TAC Tyr	TCC Ser	TAC Tyr	CGT Arg 455	CTG Leu	GAG Glu	1514
ATT Ile	GTC Val	AGT Ser 460	GAT Asp	GGA Gly	AAA Lys	TAC Tyr	GGA Gly 465	GCC Ala	CGA Arg	GAC Asp	CCT Pro	GAC Asp 470	ACG Thr	AAG Lys	GCC Ala	1562
TGG Trp	AAT Asn 475	GGC Gly	ATG Met	GTG Val	GGA Gly	GAG Glu 480	CTG Leu	GTC Val	TAT Tyr	GGA Gly 485	AGA Arg	GCA Ala	GAT Asp	GTG Val	GCT Ala	1610
GTG Val 490	GCT Ala	CCC Pro	TTA Leu	ACT Thr	ATC Ile 495	ACT Thr	TTG Leu	GTC Val	CGG Arg	GAA Glu 500	GAA Glu	GTT Val	ATA Ile	GAT Asp	TTC Phe 505	1658
TCC Ser	AAA Lys	CCA Pro	TTT Phe	ATG Met 510	AGT Ser	TTG Leu	GGG Gly	ATC Ile	TCC Ser 515	ATC Ile	ATG Met	ATT Ile	AAA Lys	AAA Lys 520	CCA Pro	1706
CAG Gln	AAA Lys	TCC Ser	AAG Lys 525	CCG Pro	GGT Gly	GTC Val	TTC Phe	TCC Ser 530	TTC Phe	CTT Leu	GAT Asp	CCT Pro	TTG Leu 535	GCT Ala	TAT Tyr	1754
GAG Glu	ATT Ile	TGG Trp 540	ATG Met	TGC Cys	ATT Ile	GTT Val	TTT Phe 545	GCC Ala	TAC Tyr	ATT Ile	GGA Gly 550	GTG Val	AGT Ser	GTT Val	GTC Val	1802
CTC Leu	TTC Phe 555	CTG Leu	GTC Val	AGC Ser	CGC Arg	TTC Phe 560	AGT Ser	CCC Pro	TAT Tyr	GAA Glu	TGG Trp 565	CAC His	AGT Ser	GAA Glu	GAG Glu	1850
TTT Phe 570	GAG Glu	GAA Glu	GGA Gly	CGG Arg	GAC Asp 575	CAG Gln	ACA Thr	ACC Thr	AGT Ser	GAC Asp 580	CAG Gln	TCC Ser	AAT Asn	GAG Glu	TTT Phe 585	1898
GGG Gly	ATA Ile	TTC Phe	AAC Asn	AGT Ser 590	TTG Leu	TGG Trp	TTC Phe	TCC Ser 595	CTG Leu	GGA Gly	GCC Ala	TTC Phe	ATG Met	CAG Gln 600	CAA Gln	1946
GGA Gly	TGT Cys	GAC Asp	ATT Ile 605	TCT Ser	CCC Pro	AGG Arg	TCC Ser 610	CTG Leu	TCT Ser	GGT Gly	CGC Arg	ATC Ile	GTT Val 615	GGT Gly	GGC Gly	1994
GTC Val	TGG Trp 620	TGG Trp	TTC Phe	TTC Phe	ACC Thr	TTA Leu	ATC Ile 625	ATC Ile	ATC Ile	TCC Ser	TCA Ser	TAT Tyr 630	ACA Thr	GCC Ala	AAT Asn	2042
CTG Leu	GCC Ala 635	GCC Ala	TTC Phe	CTG Leu	ACC Thr 640	GTG Val 640	GAG Glu	AGG Arg	ATG Met	GTG Val 645	TCT Ser 645	CCC Pro	ATT Ile	GAG Glu	AGT Ser	2090
GCA Ala 650	GAG Glu	GAC Asp	CTA Leu	GCG Ala	AAG Lys 655	CAG Gln	ACA Thr	GAA Glu	ATT Ile 660	GCC Ala 660	TAC Tyr	GGG Gly	ACG Thr	CTG Leu	GAA Glu 665	2138
GCA Ala	GGA Gly	TCT Ser	ACT Thr	AAG Lys 670	GAG Glu	TTC Phe	TTC Phe	AGG Arg 675	AGG Arg	TCT Ser	AAA Lys	ATT Ile	GCT Ala	GTG Val 680	TTT Phe	2186
GAG Glu	AAG Lys	ATG Met 685	TGG Trp	ACA Thr	TAC Tyr	ATG Met	AAG Lys	TCA Ser 690	GCA Ala	GAG Glu	CCA Pro	TCA Ser	GTT Val 695	TTT Phe	GTG Val	2234
CGG Arg	ACC Thr	ACA Thr 700	GAG Glu	GAG Glu	GGG Gly	ATG Met 705	ATT Ile	CGA Arg	GTG Val	AGG Arg	AAA Lys 710	TCC Ser 710	AAA Lys	GGC Gly	AAA Lys	2282
TAT Tyr	GCC Ala 715	TAC Tyr	CTC Leu	CTG Leu	GAG Glu 720	TCC Ser	ACC Thr	ATG Met	AAT Asn	GAG Glu 725	TAC Tyr 725	ATT Ile	GAG Glu	CAG Gln	CGG Arg	2330
AAA Lys 730	CCC Pro	TGT Cys	GAC Asp	ACC Thr	ATG Met 735	AAG Lys	GTG Val	GGA Gly	GGT Gly 740	AAC Asn 740	TTG Leu	GAT Asp	TCC Ser	AAA Lys	GGC Gly 745	2378

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TAT	GGC	ATT	GCA	ACA	CCC	AAG	GGG	TCT	GCC	CTG	GGA	AAT	CCA	GTA	AAC	2426
Tyr	Gly	Ile	Ala	Thr	Pro	Lys	Gly	Ser	Ala	Leu	Gly	Asn	Pro	Val	Asn	
				750					755					760		
CTG	GCA	GTG	TTA	AAA	CTA	AAC	GAG	CAG	GGG	CTT	TTG	GAC	AAA	TTG	AAA	2474
Leu	Ala	Val	Leu	Lys	Leu	Asn	Glu	Gln	Gly	Leu	Leu	Asp	Lys	Leu	Lys	
			765					770					775			
AAC	AAA	TGG	TGG	TAC	GAC	AAG	GGC	GAG	TGC	GGC	AGC	GGG	GGA	GGT	GAT	2522
Asn	Lys	Trp	Trp	Tyr	Asp	Lys	Gly	Glu	Cys	Gly	Ser	Gly	Gly	Gly	Asp	
		780					785					790				
TCC	AAG	GAC	AAG	ACA	AGC	GCT	CTG	AGC	CTC	AGC	AAT	GTG	GCA	GGC	GTG	2570
Ser	Lys	Asp	Lys	Thr	Ser	Ala	Leu	Ser	Leu	Ser	Asn	Val	Ala	Gly	Val	
	795					800					805					
TTC	TAC	ATC	CTG	ATC	GGA	GGA	CTT	GGA	CTA	GCC	ATG	CTG	GTT	GCC	TTA	2618
Phe	Tyr	Ile	Leu	Ile	Gly	Gly	Leu	Gly	Leu	Ala	Met	Leu	Val	Ala	Leu	
810					815					820					825	
ATC	GAG	TTC	TGC	TAC	AAA	TCC	CGT	AGT	GAA	TCC	AAG	CGG	ATG	AAG	GGT	2666
Ile	Glu	Phe	Cys	Tyr	Lys	Ser	Arg	Ser	Glu	Ser	Lys	Arg	Met	Lys	Gly	
				830					835					840		
TTT	TGT	TTG	ATC	CCA	CAG	CAA	TCC	ATC	AAC	GAA	GCC	ATA	CGG	ACA	TCG	2714
Phe	Cys	Leu	Ile	Pro	Gln	Gln	Ser	Ile	Asn	Glu	Ala	Ile	Arg	Thr	Ser	
			845					850					855			
ACC	CTC	CCC	CGC	AAC	AGC	GGG	GCA	GGA	GCC	AGC	AGC	GGC	GGC	AGT	GGA	2762
Thr	Leu	Pro	Arg	Asn	Ser	Gly	Ala	Gly	Ala	Ser	Ser	Gly	Gly	Ser	Gly	
		860					865					870				
GAG	AAT	GGT	CGG	GTG	GTC	AGC	CAT	GAC	TTC	CCC	AAG	TCC	ATG	CAA	TCG	2810
Glu	Asn	Gly	Arg	Val	Val	Ser	His	Asp	Phe	Pro	Lys	Ser	Met	Gln	Ser	
	875					880					885					
ATT	CCT	TGC	ATG	AGC	CAC	AGT	TCA	GGG	ATG	CCC	TTG	GGA	GCC	ACG	GGA	2858
Ile	Pro	Cys	Met	Ser	His	Ser	Ser	Gly	Met	Pro	Leu	Gly	Ala	Thr	Gly	
890					895					900					905	
TTG	TA	ACTGGAGC	AGATGGAGAC	CCCTTGGGGA	GCAGGCTCGG	CTCCCCAGCC										2911
Leu																
CCATCCCAA	CCCTTCAGTG	CCAAAAACAA	CAAAA													2946

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Gln	His	Ile	Phe	Ala	Phe	Phe	Cys	Thr	Gly	Phe	Leu	Gly	Ala	Val	
1				5					10					15		
Val	Gly	Ala	Asn	Phe	Pro	Asn	Asn	Ile	Gln	Ile	Gly	Gly	Leu	Phe	Pro	
			20					25					30			
Asn	Gln	Gln	Ser	Gln	Glu	His	Ala	Ala	Phe	Arg	Phe	Ala	Leu	Ser	Gln	
		35					40					45				
Leu	Thr	Glu	Pro	Pro	Lys	Leu	Leu	Pro	Gln	Ile	Asp	Ile	Val	Asn	Ile	
	50					55					60					
Ser	Asp	Ser	Phe	Glu	Met	Thr	Tyr	Arg	Phe	Cys	Ser	Gln	Phe	Ser	Lys	
	65				70					75					80	
Gly	Val	Tyr	Ala	Ile	Phe	Gly	Phe	Tyr	Glu	Arg	Arg	Thr	Val	Asn	Met	
			85					90						95		
Leu	Thr	Ser	Phe	Cys	Gly	Ala	Leu	His	Val	Cys	Phe	Ile	Thr	Pro	Ser	
			100					105					110			
Phe	Pro	Val	Asp	Thr	Ser	Asn	Gln	Phe	Val	Leu	Gln	Leu	Arg	Pro	Glu	

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115					120					125					
Leu	Gln	Asp	Ala	Leu	Ile	Ser	Ile	Ile	Asp	His	Tyr	Lys	Trp	Gln	Lys
	130					135					140				
Phe	Val	Tyr	Ile	Tyr	Asp	Ala	Asp	Arg	Gly	Leu	Ser	Val	Leu	Gln	Lys
145					150					155					160
Val	Leu	Asp	Thr	Ala	Ala	Glu	Lys	Asn	Trp	Gln	Val	Thr	Ala	Val	Asn
				165					170					175	
Ile	Leu	Thr	Thr	Thr	Glu	Glu	Gly	Tyr	Arg	Met	Leu	Phe	Gln	Asp	Leu
			180					185					190		
Glu	Lys	Lys	Lys	Glu	Arg	Leu	Val	Val	Val	Asp	Cys	Glu	Ser	Glu	Arg
		195					200					205			
Leu	Asn	Ala	Ile	Leu	Gly	Gln	Ile	Ile	Lys	Leu	Glu	Lys	Asn	Gly	Ile
	210					215					220				
Gly	Tyr	His	Tyr	Ile	Leu	Ala	Asn	Leu	Gly	Phe	Met	Asp	Ile	Asp	Leu
225				230						235					240
Asn	Lys	Phe	Lys	Glu	Ser	Gly	Ala	Asn	Val	Thr	Gly	Phe	Gln	Leu	Val
				245					250					255	
Asn	Tyr	Thr	Asp	Thr	Ile	Pro	Ala	Lys	Ile	Met	Gln	Gln	Trp	Lys	Asn
			260					265					270		
Ser	Asp	Ala	Arg	Asp	His	Thr	Arg	Val	Asp	Trp	Lys	Arg	Pro	Lys	Tyr
		275					280					285			
Thr	Ser	Ala	Leu	Thr	Tyr	Asp	Gly	Val	Lys	Val	Met	Ala	Glu	Ala	Phe
	290					295					300				
Gln	Ser	Leu	Arg	Arg	Gln	Arg	Ile	Asp	Ile	Ser	Arg	Arg	Gly	Asn	Ala
305				310						315					320
Gly	Asp	Cys	Leu	Ala	Asn	Pro	Ala	Val	Pro	Trp	Gly	Gln	Gly	Ile	Asp
				325					330					335	
Ile	Gln	Arg	Ala	Leu	Gln	Gln	Val	Arg	Phe	Glu	Gly	Leu	Thr	Gly	Asn
			340					345					350		
Val	Gln	Phe	Asn	Glu	Lys	Gly	Arg	Arg	Thr	Asn	Tyr	Thr	Leu	His	Val
		355					360					365			
Ile	Glu	Met	Lys	His	Asp	Ser	Ile	Arg	Lys	Ile	Gly	Tyr	Trp	Asn	Glu
	370				375					380					
Asp	Asp	Lys	Phe	Val	Pro	Ala	Ala	Thr	Asp	Ala	Gln	Ala	Gly	Gly	Asp
385				390						395					400
Asn	Ser	Ser	Val	Gln	Asn	Arg	Thr	Tyr	Ile	Val	Thr	Thr	Ile	Leu	Glu
			405						410					415	
Asp	Pro	Tyr	Val	Met	Leu	Lys	Lys	Asn	Ala	Asn	Gln	Phe	Glu	Gly	Asn
			420					425					430		
Asp	Arg	Tyr	Glu	Gly	Tyr	Cys	Val	Glu	Leu	Ala	Ala	Glu	Ile	Ala	Lys
		435					440					445			
His	Val	Gly	Tyr	Ser	Tyr	Arg	Leu	Glu	Ile	Val	Ser	Asp	Gly	Lys	Tyr
	450				455						460				
Gly	Ala	Arg	Asp	Pro	Asp	Thr	Lys	Ala	Trp	Asn	Gly	Met	Val	Gly	Glu
465				470						475					480
Leu	Val	Tyr	Gly	Arg	Ala	Asp	Val	Ala	Val	Ala	Pro	Leu	Thr	Ile	Thr
				485					490					495	
Leu	Val	Arg	Glu	Glu	Val	Ile	Asp	Phe	Ser	Lys	Pro	Phe	Met	Ser	Leu
			500					505					510		
Gly	Ile	Ser	Ile	Met	Ile	Lys	Lys	Pro	Gln	Lys	Ser	Lys	Pro	Gly	Val
		515				520						525			
Phe	Ser	Phe	Leu	Asp	Pro	Leu	Ala	Tyr	Glu	Ile	Trp	Met	Cys	Ile	Val
	530					535					540				

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Phe 545	Ala	Tyr	Ile	Gly	Val 550	Ser	Val	Val	Leu	Phe 555	Leu	Val	Ser	Arg	Phe 560
Ser	Pro	Tyr	Glu	Trp 565	His	Ser	Glu	Glu	Phe 570	Glu	Glu	Gly	Arg	Asp 575	Gln
Thr	Thr	Ser	Asp 580	Gln	Ser	Asn	Glu	Phe 585	Gly	Ile	Phe	Asn	Ser 590	Leu	Trp
Phe	Ser	Leu 595	Gly	Ala	Phe	Met	Gln 600	Gln	Gly	Cys	Asp	Ile 605	Ser	Pro	Arg
Ser	Leu 610	Ser	Gly	Arg	Ile	Val 615	Gly	Gly	Val	Trp	Trp 620	Phe	Phe	Thr	Leu
Ile 625	Ile	Ile	Ser	Ser	Tyr 630	Thr	Ala	Asn	Leu	Ala 635	Ala	Phe	Leu	Thr	Val 640
Glu	Arg	Met	Val	Ser 645	Pro	Ile	Glu	Ser	Ala 650	Glu	Asp	Leu	Ala	Lys 655	Gln
Thr	Glu	Ile	Ala 660	Tyr	Gly	Thr	Leu	Glu 665	Ala	Gly	Ser	Thr	Lys 670	Glu	Phe
Phe	Arg	Arg 675	Ser	Lys	Ile	Ala	Val 680	Phe	Glu	Lys	Met	Trp 685	Thr	Tyr	Met
Lys 690	Ser	Ala	Glu	Pro	Ser	Val 695	Phe	Val	Arg	Thr	Thr 700	Glu	Glu	Gly	Met
Ile 705	Arg	Val	Arg	Lys	Ser 710	Lys	Gly	Lys	Tyr	Ala 715	Tyr	Leu	Leu	Glu	Ser 720
Thr	Met	Asn	Glu	Tyr 725	Ile	Glu	Gln	Arg	Lys 730	Pro	Cys	Asp	Thr	Met 735	Lys
Val	Gly	Gly	Asn 740	Leu	Asp	Ser	Lys	Gly 745	Tyr	Gly	Ile	Ala	Thr 750	Pro	Lys
Gly	Ser	Ala 755	Leu	Gly	Asn	Pro	Val 760	Asn	Leu	Ala	Val 765	Leu	Lys	Leu	Asn
Glu	Gln 770	Gly	Leu	Leu	Asp	Lys 775	Leu	Lys	Asn	Lys	Trp 780	Trp	Tyr	Asp	Lys
Gly 785	Glu	Cys	Gly	Ser	Gly 790	Gly	Gly	Asp	Ser	Lys 795	Asp	Lys	Thr	Ser	Ala 800
Leu	Ser	Leu	Ser	Asn 805	Val	Ala	Gly	Val	Phe 810	Tyr	Ile	Leu	Ile	Gly 815	Gly
Leu	Gly	Leu	Ala 820	Met	Leu	Val	Ala	Leu 825	Ile	Glu	Phe	Cys	Tyr 830	Lys	Ser
Arg	Ser	Glu 835	Ser	Lys	Arg	Met	Lys 840	Gly	Phe	Cys	Leu	Ile 845	Pro	Gln	Gln
Ser	Ile 850	Asn	Glu	Ala	Ile	Arg 855	Thr	Ser	Thr	Leu	Pro 860	Arg	Asn	Ser	Gly
Ala 865	Gly	Ala	Ser	Ser	Gly 870	Gly	Ser	Gly	Glu	Asn 875	Gly	Arg	Val	Val	Ser 880
His	Asp	Phe	Pro	Lys 885	Ser	Met	Gln	Ser	Ile 890	Pro	Cys	Met	Ser	His 895	Ser
Ser	Gly	Met	Pro	Leu	Gly	Ala	Thr	Gly 900	Leu						

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2955 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA to mRNA

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(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) DEVELOPMENTAL STAGE: Adult
- (C) TISSUE TYPE: Brain

(i x) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 28..2676

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTTGTCGACG	CTCTACTTTT	CTTGGAA	ATG	CAA	AAG	ATT	ATG	CAT	GTT	TCT						51
			Met	Gln	Lys	Ile	Met	His	Val	Ser						
			1						5							
GTC	CTC	CTT	TCT	CCT	GTT	TTA	TGG	GGA	CTG	ATT	TTT	GGT	GTC	TCT	TCT	99
Val	Leu	Leu	Ser	Pro	Val	Leu	Trp	Gly	Leu	Ile	Phe	Gly	Val	Ser	Ser	
	10					15					20					
AAC	AGC	ATA	CAG	ATA	GGG	GGG	CTA	TTT	CCT	AGG	GGC	GCC	GAT	CAA	GAA	147
Asn	Ser	Ile	Gln	Ile	Gly	Gly	Leu	Phe	Pro	Arg	Gly	Ala	Asp	Gln	Glu	
25					30				35						40	
TAC	AGT	GCA	TTT	CGA	GTA	GGG	ATG	GTT	CAG	TTT	TCC	ACT	TCG	GAG	TTC	195
Tyr	Ser	Ala	Phe	Arg	Val	Gly	Met	Val	Gln	Phe	Ser	Thr	Ser	Glu	Phe	
				45					50					55		
AGA	CTG	ACA	CCC	CAC	ATC	GAC	AAT	TTG	GAG	GTG	GCA	AAC	AGC	TTC	GCA	243
Arg	Leu	Thr	Pro	His	Ile	Asp	Asn	Leu	Glu	Val	Ala	Asn	Ser	Phe	Ala	
			60					65					70			
GTC	ACT	AAT	GCT	TTC	TGC	TCC	CAG	TTT	TCG	AGA	GGA	GTC	TAT	GCT	ATT	291
Val	Thr	Asn	Ala	Phe	Cys	Ser	Gln	Phe	Ser	Arg	Gly	Val	Tyr	Ala	Ile	
		75					80					85				
TTT	GGA	TTT	TAT	GAC	AAG	AAG	TCT	GTA	AAT	ACC	ATC	ACA	TCA	TTT	TGC	339
Phe	Gly	Phe	Tyr	Asp	Lys	Lys	Ser	Val	Asn	Thr	Ile	Thr	Ser	Phe	Cys	
	90					95					100					
GGA	ACA	CTC	CAC	GTC	TCC	TTC	ATC	ACT	CCC	AGC	TTC	CCA	ACA	GAT	GGC	387
Gly	Thr	Leu	His	Val	Ser	Phe	Ile	Thr	Pro	Ser	Phe	Pro	Thr	Asp	Gly	
105					110					115					120	
ACA	CAT	CCA	TTT	GTC	ATT	CAG	ATG	AGA	CCC	GAC	CTC	AAA	GGA	GCT	CTC	435
Thr	His	Pro	Phe	Val	Ile	Gln	Met	Arg	Pro	Asp	Leu	Lys	Gly	Ala	Leu	
				125					130					135		
CIT	AGC	TTG	ATT	GAA	TAC	TAT	CAA	TGG	GAC	AAG	TTT	GCA	TAC	CTC	TAT	483
Leu	Ser	Leu	Ile	Glu	Tyr	Tyr	Gln	Trp	Asp	Lys	Phe	Ala	Tyr	Leu	Tyr	
			140					145					150			
GAC	AGT	GAC	AGA	GGC	TTA	TCA	ACA	CTG	CAA	GCT	GTG	CTG	GAT	TCT	GCT	531
Asp	Ser	Asp	Arg	Gly	Leu	Ser	Thr	Leu	Gln	Ala	Val	Leu	Asp	Ser	Ala	
		155					160				165					
GCT	GAA	AAG	AAA	TGG	CAA	GTG	ACT	GCT	ATC	AAT	GTG	GGA	AAC	ATT	AAC	579
Ala	Glu	Lys	Lys	Trp	Gln	Val	Thr	Ala	Ile	Asn	Val	Gly	Asn	Ile	Asn	
	170					175					180					
AAT	GAC	AAG	AAA	GAT	GAG	ATG	TAC	CGA	TCA	CTT	TTT	CAA	GAT	CTG	GAG	627
Asn	Asp	Lys	Lys	Asp	Glu	Met	Tyr	Arg	Ser	Leu	Phe	Gln	Asp	Leu	Glu	
	185				190						195				200	
TTA	AAA	AAG	GAA	CGG	CGT	GTA	ATT	CTG	GAC	TGT	GAA	AGG	GAT	AAA	GTA	675
Leu	Lys	Lys	Glu	Arg	Arg	Val	Ile	Leu	Asp	Cys	Glu	Arg	Asp	Lys	Val	
				205					210					215		
AAC	GAC	ATT	GTA	GAC	CAG	GTT	ATT	ACC	ATT	GGA	AAA	CAC	GTT	AAA	GGG	723
Asn	Asp	Ile	Val	Asp	Gln	Val	Ile	Thr	Ile	Gly	Lys	His	Val	Lys	Gly	
			220					225					230			
TAC	CAC	TAC	ATC	ATT	GCA	AAT	CTG	GGA	TTT	ACT	GAT	GGA	GAC	CTA	TTA	771
Tyr	His	Tyr	Ile	Ile	Ala	Asn	Leu	Gly	Phe	Thr	Asp	Gly	Asp	Leu	Leu	
		235					240					245				
AAA	ATC	CAG	TTT	GGA	GGT	GCA	AAT	GTC	TCT	GGA	TTT	CAG	ATA	GTG	GAC	819
Lys	Ile	Gln	Phe	Gly	Gly	Ala	Asn	Val	Ser	Gly	Phe	Gln	Ile	Val	Asp	
	250					255					260					
TAT	GAT	GAT	TCG	TTG	GTA	TCT	AAA	TTT	ATA	GAA	AGA	TGG	TCA	ACA	CTG	867

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Tyr 265	Asp	Asp	Ser	Leu	Val 270	Ser	Lys	Phe	Ile	Glu 275	Arg	Trp	Ser	Thr	Leu 280	
GAA Glu	GAA Glu	AAA Lys	GAA Glu	TAC Tyr 285	CCT Pro	GGA Gly	GCT Ala	CAC His	ACA Thr 290	ACA Thr	ACA Thr	ATT Ile	AAG Lys	TAT Tyr 295	ACT Thr	915
TCT Ser	GCT Ala	CTG Leu	ACC Thr 300	TAT Tyr	GAT Asp	GCC Ala	GTT Val	CAA Gln 305	GTG Val	ATG Met	ACT Thr	GAA Glu	GCC Ala 310	TTC Phe	CGC Arg	963
AAC Asn	CTA Leu	AGG Arg 315	AAG Lys	CAA Gln	AGA Arg	ATT Ile	GAA Glu 320	ATC Ile	TCC Ser	CGA Arg	AGG Arg	GGG Gly 325	AAT Asn	GCA Ala	GGA Gly	1011
GAC Asp	TGT Cys 330	CTG Leu	GCA Ala	AAC Asn	CCA Pro	GCA Ala 335	GTG Val	CCC Pro	TGG Trp	GGA Gly	CAA Gln 340	GGT Gly	GTA Val	GAA Glu	ATA Ile	1059
GAA Glu 345	AGG Arg	GCC Ala	CTC Leu	AAA Lys	CAG Gln 350	GTT Val	CAG Gln	GTT Val	GAA Glu 355	GGT Gly	CTC Leu	TCA Ser	GGA Gly	AAT Asn	ATA Ile 360	1107
AAG Lys	TTT Phe	GAC Asp	CAG Gln	AAT Asn 365	GGA Gly	AAA Lys	AGA Arg	ATA Ile	AAC Asn 370	TAT Tyr	ACA Thr	ATT Ile	AAC Asn	ATC Ile 375	ATG Met	1155
GAG Glu	CTC Leu	AAA Lys	ACT Thr 380	AAT Asn	GGG Gly	CCC Pro	CGG Arg	AAG Lys 385	ATT Ile	GGC Gly	TAC Tyr	TGG Trp	AGT Ser 390	GAA Glu	GTG Val	1203
GAC Asp	AAA Lys 395	ATG Met	GTT Val	GTT Val	ACC Thr	CTT Leu	ACT Thr 400	GAG Glu	CTC Leu	CCT Pro	TCT Ser	GGA Gly 405	AAT Asn	GAC Asp	ACC Thr	1251
TCT Ser 410	GGG Gly	CTT Leu	GAG Glu	AAT Asn	AAG Lys 415	ACT Thr	GTT Val	GTT Val	GTC Val	ACC Thr	ACA Thr 420	ATT Ile	TTG Leu	GAA Glu	TCT Ser	1299
CCG Pro 425	TAT Tyr	GTT Val	ATG Met	ATG Met	AAG Lys 430	AAA Lys	AAT Asn	CAT His	GAA Glu	ATG Met 435	CTT Leu	GAA Glu	GGC Gly	AAT Asn	GAG Glu 440	1347
CGC Arg	TAT Tyr	GAG Glu	GGC Gly	TAC Tyr 445	TGT Cys	GTT Val	GAC Asp	CTG Leu	GCT Ala 450	GCA Ala	GAA Glu	ATC Ile	GCC Ala	AAA Lys 455	CAT His	1395
TGT Cys	GGG Gly	TTC Phe	AAG Lys 460	TAC Tyr	AAG Lys	TTG Leu	ACA Thr	ATT Ile 465	GTT Val	GGT Gly	GAT Asp	GGC Gly	AAG Lys 470	TAT Tyr	GGG Gly	1443
GCC Ala	AGG Arg	GAT Asp 475	GCA Ala	GAC Asp	ACG Thr	AAA Lys	ATT Ile 480	TGG Trp	AAT Asn	GGG Gly	ATG Met	GTT Val 485	GGA Gly	GAA Glu	CTT Leu	1491
GTA Val 490	TAT Tyr	GGG Gly	AAA Lys	GCT Ala	GAT Asp	ATT Ile 495	GCA Ala	ATT Ile	GCT Ala	CCA Pro	TTA Leu 500	ACT Thr	ATT Ile	ACC Thr	CTT Leu	1539
GTG Val 505	AGA Arg	GAA Glu	GAG Glu	GTG Val 510	ATT Ile 510	GAC Asp	TTC Phe	TCA Ser	AAG Lys 515	CCC Pro	TTC Phe	ATG Met	AGC Ser	CTC Leu	GGG Gly 520	1587
ATA Ile	TCT Ser	ATC Ile	ATG Met	ATC Ile 525	AAG Lys	AAG Lys	CCT Pro	CAG Gln	AAG Lys 530	TCC Ser	AAA Lys	CCA Pro	GGA Gly	GTG Val 535	TTT Phe	1635
TCC Ser	TTT Phe	CTT Leu	GAT Asp 540	CCT Pro	TTA Leu	GCC Ala	TAT Tyr	GAG Glu 545	ATC Ile	TGG Trp	ATG Met	TGC Cys 550	ATT Ile	GTT Val	TTT Phe	1683
GCC Ala	TAC Tyr	ATT Ile 555	GGG Gly	GTC Val	AGT Ser	GTA Val	GTT Val 560	TTA Leu	TTC Phe	CTG Leu	GTC Val	AGC Ser 565	AGA Arg	TTT Phe	AGC Ser	1731
CCC Pro 570	TAC Tyr	GAG Glu	TGG Trp	CAC His	ACT Thr	GAG Glu 575	GAG Glu	TTT Phe	GAA Glu	GAT Asp	GGA Gly 580	AGA Arg	GAA Glu	ACA Thr	CAA Gln	1779
AGT	AGT	GAA	TCA	ACT	AAT	GAA	TTT	GGG	ATT	TTT	AAT	AGT	CTC	TGG	TTT	1827

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Ser 585	Ser	Glu	Ser	Thr	Asn 590	Glu	Phe	Gly	Ile	Phe 595	Asn	Ser	Leu	Trp	Phe 600	
TCC Ser	TTG Leu	GGT Gly	GCC Ala	TTT Phe 605	ATG Met	CGG Arg	CAA Gln	GGA Gly	TGC Cys 610	GAT Asp	ATT Ile	TCG Ser	CCA Pro	AGA Arg 615	TCC Ser	1875
CTC Leu	TCT Ser	GGG Gly	CGC Arg 620	ATT Ile	GTT Val	GGA Gly	GGT Gly	GTG Val 625	TGG Trp	TGG Trp	TTC Phe	TTT Phe	ACC Thr 630	CTG Leu	ATC Ile	1923
ATA Ile	ATC Ile	TCC Ser 635	TCC Ser	TAC Tyr	ACG Thr	GCT Ala	AAC Asn 640	TTA Leu	GCT Ala	GCC Ala	TTC Phe	CTG Leu 645	ACT Thr	GTA Val	GAG Glu	1971
AGG Arg	ATG Met 650	GTG Val	TCT Ser	CCC Pro	ATC Ile	GAA Glu 655	AGT Ser	GCT Ala	GAG Glu	GAT Asp	CTT Leu 660	TCT Ser	AAG Lys	CAA Gln	ACA Thr	2019
GAA Glu 665	ATT Ile	GCT Ala	TAT Tyr	GGA Gly 670	ACA Thr	TTA Leu	GAC Asp	TCT Ser	GGC Gly	TCC Ser 675	ACT Thr	AAA Lys	GAG Glu	TTT Phe	TTC Phe 680	2067
AGG Arg	AGA Arg	TCT Ser	AAA Lys 685	ATT Ile	GCA Ala	GTG Val	TTT Phe	GAT Asp 690	AAA Lys	ATG Met	TGG Trp	ACC Thr	TAC Tyr	ATG Met 695	CGG Arg	2115
AGT Ser	GCG Ala	GAG Glu	CCC Pro 700	TCT Ser	GTG Val	TTT Phe	GTG Val	AGG Arg 705	ACT Thr	ACG Thr	GCC Ala	GAA Glu	GGG Gly 710	GTG Val	GCT Ala	2163
AGA Arg	GTG Val	CGG Arg 715	AAG Lys	TCC Ser	AAA Lys	GGG Gly	AAA Lys 720	TAT Tyr	GCC Ala	TAC Tyr	TTG Leu	TTG Leu 725	GAG Glu	TCC Ser	ACG Thr	2211
ATG Met 730	AAC Asn	GAG Glu	TAC Tyr	ATT Ile	GAG Glu	CAA Gln 735	AGG Arg	AAG Lys	CCT Pro	TGC Cys	GAC Asp 740	ACC Thr	ATG Met	AAA Lys	GTT Val	2259
GGT Gly 745	GGA Gly	AAC Asn	CTG Leu	GAT Asp	TCC Ser 750	AAA Lys	GGC Gly	TAT Tyr	GGC Gly	ATC Ile 755	GCA Ala	ACA Thr	CCT Pro	AAA Lys	GGA Gly 760	2307
TCC Ser	TCA Ser	TTA Leu	GGA Gly 765	ACC Thr	CCA Pro	GTA Val	AAT Asn	CTT Leu	GCA Ala 770	GTA Val	TTG Leu	AAA Lys	CTC Leu	AGT Ser 775	GAG Glu	2355
CAA Gln	GGC Gly	GTC Val 780	TTA Leu	GAC Asp	AAG Lys	CTG Leu	AAA Lys 785	AAC Asn	AAA Lys	TGG Trp	TGG Trp	TAC Tyr	GAT Asp 790	AAA Lys	GGT Gly	2403
GAA Glu	TGT Cys	GGA Gly 795	GCC Ala	AAG Lys	GAC Asp	TCT Ser	GGA Gly 800	AGT Ser	AAG Lys	GAA Glu	AAG Lys	ACC Thr 805	AGT Ser	GCC Ala	CTC Leu	2451
AGT Ser	CTG Leu 810	AGC Ser	AAC Asn	GTT Val	GCT Ala	GGA Gly 815	GTA Val	TTC Phe	TAC Tyr	ATC Ile	CTT Leu 820	GTC Val	GGG Gly	GGC Gly	CTT Leu	2499
GGT Gly 825	TTG Leu	GCA Ala	ATG Met	CTG Leu	GTG Val 830	GCT Ala	TTG Leu	ATT Ile	GAG Glu	TTC Phe 835	TGT Cys	TAC Tyr	AAG Lys	TCA Ser	AGG Arg 840	2547
GCC Ala	GAG Glu	GCG Ala	AAA Lys 845	CGA Arg	ATG Met	AAG Lys	GTG Val	GCA Ala	AAG Lys 850	AAT Asn	GCA Ala	CAG Gln	AAT Asn 855	ATT Ile	AAC Asn	2595
CCA Pro	TCT Ser	TCC Ser	TCG Ser 860	CAG Gln	AAT Asn	TCA Ser	CAG Gln	AAT Asn 865	TTT Phe	GCA Ala	ACT Thr	TAT Tyr	AAG Lys 870	GAA Glu	GGT Gly	2643
TAC Tyr	AAC Asn 875	GTA Val	TAT Tyr	GGC Gly	ATC Ile	GAA Glu	AGT Ser	GTT Val 880	AAA Lys	ATT Ile	TAGGGGATGA CCTTGAAATG				2696	
ATGCCATGAG		GAACAAGGCA		AGGCTGTCAA		TTACAGGAAG		TACTGGAGAA		AATGGACGTG		2756				
TTATGACTCC		AGAATTTCCC		AAAGCAGTGC		ATGCTGTCCC		TTACGTGAGT		CCTGGCATGG		2816				
GAATGAATGT		CAGTGTGACT		GATCTCTCGT		GATTGATAAG		AACCTTTTGA		GTGCCTTACA		2876				

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CAATGGTTTT CTGTGTTTA TTGTCAAAGT GGTGAGAGGC ATCCAGTATC TTGAAGACTT 2936
 TTCTTTCAGC CAAGAATTC 2955

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Gln	Lys	Ile	Met	His	Val	Ser	Val	Leu	Leu	Ser	Pro	Val	Leu	Trp
1				5					10					15	
Gly	Leu	Ile	Phe	Gly	Val	Ser	Ser	Asn	Ser	Ile	Gln	Ile	Gly	Gly	Leu
			20					25					30		
Phe	Pro	Arg	Gly	Ala	Asp	Gln	Glu	Tyr	Ser	Ala	Phe	Arg	Val	Gly	Met
		35					40					45			
Val	Gln	Phe	Ser	Thr	Ser	Glu	Phe	Arg	Leu	Thr	Pro	His	Ile	Asp	Asn
	50					55					60				
Leu	Glu	Val	Ala	Asn	Ser	Phe	Ala	Val	Thr	Asn	Ala	Phe	Cys	Ser	Gln
65					70					75					80
Phe	Ser	Arg	Gly	Val	Tyr	Ala	Ile	Phe	Gly	Phe	Tyr	Asp	Lys	Lys	Ser
				85					90					95	
Val	Asn	Thr	Ile	Thr	Ser	Phe	Cys	Gly	Thr	Leu	His	Val	Ser	Phe	Ile
			100					105					110		
Thr	Pro	Ser	Phe	Pro	Thr	Asp	Gly	Thr	His	Pro	Phe	Val	Ile	Gln	Met
		115					120					125			
Arg	Pro	Asp	Leu	Lys	Gly	Ala	Leu	Leu	Ser	Leu	Ile	Glu	Tyr	Tyr	Gln
	130					135					140				
Trp	Asp	Lys	Phe	Ala	Tyr	Leu	Tyr	Asp	Ser	Asp	Arg	Gly	Leu	Ser	Thr
145					150					155					160
Leu	Gln	Ala	Val	Leu	Asp	Ser	Ala	Ala	Glu	Lys	Lys	Trp	Gln	Val	Thr
				165					170					175	
Ala	Ile	Asn	Val	Gly	Asn	Ile	Asn	Asn	Asp	Lys	Lys	Asp	Glu	Met	Tyr
			180					185					190		
Arg	Ser	Leu	Phe	Gln	Asp	Leu	Glu	Leu	Lys	Lys	Glu	Arg	Arg	Val	Ile
		195					200					205			
Leu	Asp	Cys	Glu	Arg	Asp	Lys	Val	Asn	Asp	Ile	Val	Asp	Gln	Val	Ile
	210					215					220				
Thr	Ile	Gly	Lys	His	Val	Lys	Gly	Tyr	His	Tyr	Ile	Ile	Ala	Asn	Leu
225					230					235					240
Gly	Phe	Thr	Asp	Gly	Asp	Leu	Leu	Lys	Ile	Gln	Phe	Gly	Gly	Ala	Asn
				245					250					255	
Val	Ser	Gly	Phe	Gln	Ile	Val	Asp	Tyr	Asp	Asp	Ser	Leu	Val	Ser	Lys
			260					265					270		
Phe	Ile	Glu	Arg	Trp	Ser	Thr	Leu	Glu	Glu	Lys	Glu	Tyr	Pro	Gly	Ala
		275					280					285			
His	Thr	Thr	Thr	Ile	Lys	Tyr	Thr	Ser	Ala	Leu	Thr	Tyr	Asp	Ala	Val
	290					295					300				
Gln	Val	Met	Thr	Glu	Ala	Phe	Arg	Asn	Leu	Arg	Lys	Gln	Arg	Ile	Glu
305					310					315					320
Ile	Ser	Arg	Arg	Gly	Asn	Ala	Gly	Asp	Cys	Leu	Ala	Asn	Pro	Ala	Val
				325					330					335	

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Pro	Trp	Gly	Gln 340	Gly	Val	Glu	Ile	Glu 345	Arg	Ala	Leu	Lys	Gln 350	Val	Gln
Val	Glu	Gly 355	Leu	Ser	Gly	Asn	Ile 360	Lys	Phe	Asp	Gln	Asn 365	Gly	Lys	Arg
Ile	Asn 370	Tyr	Thr	Ile	Asn	Ile 375	Met	Glu	Leu	Lys	Thr 380	Asn	Gly	Pro	Arg
Lys 385	Ile	Gly	Tyr	Trp	Ser 390	Glu	Val	Asp	Lys	Met 395	Val	Val	Thr	Leu	Thr 400
Glu	Leu	Pro	Ser 405	Gly	Asn	Asp	Thr	Ser	Gly 410	Leu	Glu	Asn	Lys	Thr 415	Val
Val	Val	Thr 420	Thr	Ile	Leu	Glu	Ser	Pro 425	Tyr	Val	Met	Met	Lys 430	Lys	Asn
His	Glu	Met 435	Leu	Glu	Gly	Asn	Glu 440	Arg	Tyr	Glu	Gly	Tyr 445	Cys	Val	Asp
Leu	Ala 450	Ala	Glu	Ile	Ala	Lys 455	His	Cys	Gly	Phe	Lys 460	Tyr	Lys	Leu	Thr
Ile 465	Val	Gly	Asp	Gly	Lys 470	Tyr	Gly	Ala	Arg	Asp 475	Ala	Asp	Thr	Lys	Ile 480
Trp	Asn	Gly	Met 485	Val	Gly	Glu	Leu	Val 490	Tyr	Gly	Lys	Ala	Asp	Ile 495	Ala
Ile	Ala	Pro	Leu 500	Thr	Ile	Thr	Leu	Val 505	Arg	Glu	Glu	Val	Ile 510	Asp	Phe
Ser	Lys	Pro 515	Phe	Met	Ser	Leu	Gly 520	Ile	Ser	Ile	Met	Ile 525	Lys	Lys	Pro
Gln	Lys 530	Ser	Lys	Pro	Gly	Val 535	Phe	Ser	Phe	Leu	Asp 540	Pro	Leu	Ala	Tyr
Glu 545	Ile	Trp	Met	Cys	Ile 550	Val	Phe	Ala	Tyr	Ile 555	Gly	Val	Ser	Val	Val 560
Leu	Phe	Leu	Val 565	Ser	Arg	Phe	Ser	Pro	Tyr 570	Glu	Trp	His	Thr	Glu 575	Glu
Phe	Glu	Asp 580	Gly	Arg	Glu	Thr	Gln 585	Ser	Ser	Glu	Ser	Thr	Asn 590	Glu	Phe
Gly	Ile	Phe 595	Asn	Ser	Leu	Trp	Phe 600	Ser	Leu	Gly	Ala	Phe 605	Met	Arg	Gln
Gly	Cys 610	Asp	Ile	Ser	Pro	Arg 615	Ser	Leu	Ser	Gly	Arg 620	Ile	Val	Gly	Gly
Val 625	Trp	Trp	Phe	Phe	Thr 630	Leu	Ile	Ile	Ile	Ser 635	Ser	Tyr	Thr	Ala	Asn 640
Leu	Ala	Ala	Phe 645	Leu	Thr	Val	Glu	Arg	Met 650	Val	Ser	Pro	Ile	Glu 655	Ser
Ala	Glu	Asp 660	Leu	Ser	Lys	Gln	Thr 665	Glu	Ile	Ala	Tyr	Gly	Thr 670	Leu	Asp
Ser	Gly	Ser 675	Thr	Lys	Glu	Phe	Phe 680	Arg	Arg	Ser	Lys	Ile 685	Ala	Val	Phe
Asp 690	Lys	Met	Trp	Thr	Tyr	Met 695	Arg	Ser	Ala	Glu	Pro 700	Ser	Val	Phe	Val
Arg 705	Thr	Thr	Ala	Glu	Gly 710	Val	Ala	Arg	Val	Arg 715	Lys	Ser	Lys	Gly	Lys 720
Tyr	Ala	Tyr	Leu 725	Leu	Glu	Ser	Thr	Met	Asn 730	Glu	Tyr	Ile	Glu	Gln 735	Arg
Lys	Pro	Cys	Asp 740	Thr	Met	Lys	Val	Gly 745	Gly	Asn	Leu	Asp	Ser 750	Lys	Gly
Tyr	Gly	Ile 755	Ala	Thr	Pro	Lys	Gly 760	Ser	Ser	Leu	Gly	Thr 765	Pro	Val	Asn

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Leu Ala Val Leu Lys Leu Ser Glu Gln Gly Val Leu Asp Lys Leu Lys
 770 775 780

Asn Lys Trp Trp Tyr Asp Lys Gly Glu Cys Gly Ala Lys Asp Ser Gly
 785 790 795 800

Ser Lys Glu Lys Thr Ser Ala Leu Ser Leu Ser Asn Val Ala Gly Val
 805 810 815

Phe Tyr Ile Leu Val Gly Gly Leu Gly Leu Ala Met Leu Val Ala Leu
 820 825 830

Ile Glu Phe Cys Tyr Lys Ser Arg Ala Glu Ala Lys Arg Met Lys Val
 835 840 845

Ala Lys Asn Ala Gln Asn Ile Asn Pro Ser Ser Ser Gln Asn Ser Gln
 850 855 860

Asn Phe Ala Thr Tyr Lys Glu Gly Tyr Asn Val Tyr Gly Ile Glu Ser
 865 870 875 880

Val Lys Ile

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2955 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA to mRNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) DEVELOPMENTAL STAGE: Adult
- (C) TISSUE TYPE: Brain

(i x) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 28..2676

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TTTGTGCGACG CTCTACTTTT CTTGGAA ATG CAA AAG ATT ATG CAT GTT TCT 51
 Met Gln Lys Ile Met His Val Ser
 1 5

GTC CTC CTT TCT CCT GTT TTA TGG GGA CTG ATT TTT GGT GTC TCT TCT 99
 Val Leu Leu Ser Pro Val Leu Trp Gly Leu Ile Phe Gly Val Ser Ser
 10 15 20

AAC AGC ATA CAG ATA GGG GGG CTA TTT CCT AGG GGC GCC GAT CAA GAA 147
 Asn Ser Ile Gln Ile Gly Gly Leu Phe Pro Arg Gly Ala Asp Gln Glu
 25 30 35 40

TAC AGT GCA TTT CGA GTA GGG ATG GTT CAG TTT TCC ACT TCG GAG TTC 195
 Tyr Ser Ala Phe Arg Val Gly Met Val Gln Phe Ser Thr Ser Glu Phe
 45 50 55

AGA CTG ACA CCC CAC ATC GAC AAT TTG GAG GTG GCA AAC AGC TTC GCA 243
 Arg Leu Thr Pro His Ile Asp Asn Leu Glu Val Ala Asn Ser Phe Ala
 60 65 70

GTC ACT AAT GCT TTC TGC TCC CAG TTT TCG AGA GGA GTC TAT GCT ATT 291
 Val Thr Asn Ala Phe Cys Ser Gln Phe Ser Arg Gly Val Tyr Ala Ile
 75 80 85

TTT GGA TTT TAT GAC AAG AAG TCT GTA AAT ACC ATC ACA TCA TTT TGC 339
 Phe Gly Phe Tyr Asp Lys Lys Ser Val Asn Thr Ile Thr Ser Phe Cys
 90 95 100

GGA ACA CTC CAC GTC TCC TTC ATC ACT CCC AGC TTC CCA ACA GAT GGC 387
 Gly Thr Leu His Val Ser Phe Ile Thr Pro Ser Phe Pro Thr Asp Gly
 105 110 115 120

ACA CAT CCA TTT GTC ATT CAG ATG AGA CCC GAC CTC AAA GGA GCT CTC 435
 Thr His Pro Phe Val Ile Gln Met Arg Pro Asp Leu Lys Gly Ala Leu

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				125					130					135					
CTT	AGC	TTG	ATT	GAA	TAC	TAT	CAA	TGG	GAC	AAG	TTT	GCA	TAC	CTC	TAT		483		
Leu	Ser	Leu	Ile	Glu	Tyr	Tyr	Gln	Trp	Asp	Lys	Phe	Ala	Tyr	Leu	Tyr				
			140					145					150						
GAC	AGT	GAC	AGA	GGC	TTA	TCA	ACA	CTG	CAA	GCT	GTG	CTG	GAT	TCT	GCT		531		
Asp	Ser	Asp	Arg	Gly	Leu	Ser	Thr	Leu	Gln	Ala	Val	Leu	Asp	Ser	Ala				
		155					160					165							
GCT	GAA	AAG	AAA	TGG	CAA	GTG	ACT	GCT	ATC	AAT	GTG	GGA	AAC	ATT	AAC		579		
Ala	Glu	Lys	Lys	Trp	Gln	Val	Thr	Ala	Ile	Asn	Val	Gly	Asn	Ile	Asn				
	170					175					180								
AAT	GAC	AAG	AAA	GAT	GAG	ATG	TAC	CGA	TCA	CTT	TTT	CAA	GAT	CTG	GAG		627		
Asn	Asp	Lys	Lys	Asp	Glu	Met	Tyr	Arg	Ser	Leu	Phe	Gln	Asp	Leu	Glu				
185				190						195					200				
TTA	AAA	AAG	GAA	CGG	CGT	GTA	ATT	CTG	GAC	TGT	GAA	AGG	GAT	AAA	GTA		675		
Leu	Lys	Lys	Glu	Arg	Arg	Val	Ile	Leu	Asp	Cys	Glu	Arg	Asp	Lys	Val				
			205						210					215					
AAC	GAC	ATT	GTA	GAC	CAG	GTT	ATT	ACC	ATT	GGA	AAA	CAC	GTT	AAA	GGG		723		
Asn	Asp	Ile	Val	Asp	Gln	Val	Ile	Thr	Ile	Gly	Lys	His	Val	Lys	Gly				
		220						225					230						
TAC	CAC	TAC	ATC	ATT	GCA	AAT	CTG	GGA	TTT	ACT	GAT	GGA	GAC	CTA	TTA		771		
Tyr	His	Tyr	Ile	Ile	Ala	Asn	Leu	Gly	Phe	Thr	Asp	Gly	Asp	Leu	Leu				
		235					240					245							
AAA	ATC	CAG	TTT	GGA	GGT	GCA	AAT	GTC	TCT	GGA	TTT	CAG	ATA	GTG	GAC		819		
Lys	Ile	Gln	Phe	Gly	Gly	Ala	Asn	Val	Ser	Gly	Phe	Gln	Ile	Val	Asp				
	250			255						260									
TAT	GAT	GAT	TCG	TTG	GTA	TCT	AAA	TTT	ATA	GAA	AGA	TGG	TCA	ACA	CTG		867		
Tyr	Asp	Asp	Ser	Leu	Val	Ser	Lys	Phe	Ile	Glu	Arg	Trp	Ser	Thr	Leu				
265				270						275					280				
GAA	GAA	AAA	GAA	TAC	CCT	GGA	GCT	CAC	ACA	ACA	ACA	ATT	AAG	TAT	ACT		915		
Glu	Glu	Lys	Glu	Tyr	Pro	Gly	Ala	His	Thr	Thr	Thr	Ile	Lys	Tyr	Thr				
			285					290						295					
TCT	GCT	CTG	ACC	TAT	GAT	GCC	GTT	CAA	GTG	ATG	ACT	GAA	GCC	TTC	CGC		963		
Ser	Ala	Leu	Thr	Tyr	Asp	Ala	Val	Gln	Val	Met	Thr	Glu	Ala	Phe	Arg				
		300						305					310						
AAC	CTA	AGG	AAG	CAA	AGA	ATT	GAA	ATC	TCC	CGA	AGG	GGG	AAT	GCA	GGA		1011		
Asn	Leu	Arg	Lys	Gln	Arg	Ile	Glu	Ile	Ser	Arg	Arg	Gly	Asn	Ala	Gly				
		315					320					325							
GAC	TGT	CTG	GCA	AAC	CCA	GCA	GTG	CCC	TGG	GGA	CAA	GGT	GTA	GAA	ATA		1059		
Asp	Cys	Leu	Ala	Asn	Pro	Ala	Val	Pro	Trp	Gly	Gln	Gly	Val	Glu	Ile				
	330						335				340								
GAA	AGG	GCC	CTC	AAA	CAG	GTT	CAG	GTT	GAA	GGT	CTC	TCA	GGA	AAT	ATA		1107		
Glu	Arg	Ala	Leu	Lys	Gln	Val	Gln	Val	Glu	Gly	Leu	Ser	Gly	Asn	Ile				
345					350					355					360				
AAG	TTT	GAC	CAG	AAT	GGA	AAA	AGA	ATA	AAC	TAT	ACA	ATT	AAC	ATC	ATG		1155		
Lys	Phe	Asp	Gln	Asn	Gly	Lys	Arg	Ile	Asn	Tyr	Thr	Ile	Asn	Ile	Met				
			365						370					375					
GAG	CTC	AAA	ACT	AAT	GGG	CCC	CGG	AAG	ATT	GGC	TAC	TGG	AGT	GAA	GTG		1203		
Glu	Leu	Lys	Thr	Asn	Gly	Pro	Arg	Lys	Ile	Gly	Tyr	Trp	Ser	Glu	Val				
		380						385					390						
GAC	AAA	ATG	GTT	GTT	ACC	CTT	ACT	GAG	CTC	CCT	TCT	GGA	AAT	GAC	ACC		1251		
Asp	Lys	Met	Val	Val	Thr	Leu	Thr	Glu	Leu	Pro	Ser	Gly	Asn	Asp	Thr				
		395					400					405							
TCT	GGG	CTT	GAG	AAT	AAG	ACT	GTT	GTT	GTC	ACC	ACA	ATT	TTG	GAA	TCT		1299		
Ser	Gly	Leu	Glu	Asn	Lys	Thr	Val	Val	Val	Thr	Thr	Ile	Leu	Glu	Ser				
	410					415					420								
CCG	TAT	GTT	ATG	ATG	AAG	AAA	AAT	CAT	GAA	ATG	CTT	GAA	GGC	AAT	GAG		1347		
Pro	Tyr	Val	Met	Met	Lys	Lys	Asn	His	Glu	Met	Leu	Glu	Gly	Asn	Glu				
425					430					435					440				
CGC	TAT	GAG	GGC	TAC	TGT	GTT	GAC	CTG	GCT	GCA	GAA	ATC	GCC	AAA	CAT		1395		
Arg	Tyr	Glu	Gly	Tyr	Cys	Val	Asp	Leu	Ala	Ala	Glu	Ile	Ala	Lys	His				

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445				450				455								
TGT	GGG	TTC	AAG	TAC	AAG	TTG	ACA	ATT	GTT	GGT	GAT	GGC	AAG	TAT	GGG	1443
Cys	Gly	Phe	Lys	Tyr	Lys	Leu	Thr	Ile	Val	Gly	Asp	Gly	Lys	Tyr	Gly	
			460					465					470			
GCC	AGG	GAT	GCA	GAC	ACG	AAA	ATT	TGG	AAT	GGG	ATG	GTT	GGA	GAA	CTT	1491
Ala	Arg	Asp	Ala	Asp	Thr	Lys	Ile	Trp	Asn	Gly	Met	Val	Gly	Glu	Leu	
		475					480					485				
GTA	TAT	GGG	AAA	GCT	GAT	ATT	GCA	ATT	GCT	CCA	TTA	ACT	ATT	ACC	CTT	1539
Val	Tyr	Gly	Lys	Ala	Asp	Ile	Ala	Ile	Ala	Pro	Leu	Thr	Ile	Thr	Leu	
	490					495					500					
GTG	AGA	GAA	GAG	GTG	ATT	GAC	TTC	TCA	AAG	CCC	TTC	ATG	AGC	CTC	GGG	1587
Val	Arg	Glu	Glu	Val	Ile	Asp	Phe	Ser	Lys	Pro	Phe	Met	Ser	Leu	Gly	
505					510					515					520	
ATA	TCT	ATC	ATG	ATC	AAG	AAG	CCT	CAG	AAG	TCC	AAA	CCA	GGA	GTG	TTT	1635
Ile	Ser	Ile	Met	Ile	Lys	Lys	Pro	Gln	Lys	Ser	Lys	Pro	Gly	Val	Phe	
				525					530					535		
TCC	TTT	CTT	GAT	CCT	TTA	GCC	TAT	GAG	ATC	TGG	ATG	TGC	ATT	GTT	TTT	1683
Ser	Phe	Leu	Asp	Pro	Leu	Ala	Tyr	Glu	Ile	Trp	Met	Cys	Ile	Val	Phe	
			540					545					550			
GCC	TAC	ATT	GGG	GTC	AGT	GTA	GTT	TTA	TTC	CTG	GTC	AGC	AGA	TTT	AGC	1731
Ala	Tyr	Ile	Gly	Val	Ser	Val	Val	Leu	Phe	Leu	Val	Ser	Arg	Phe	Ser	
		555					560					565				
CCC	TAC	GAG	TGG	CAC	ACT	GAG	GAG	TTT	GAA	GAT	GGA	AGA	GAA	ACA	CAA	1779
Pro	Tyr	Glu	Trp	His	Thr	Glu	Glu	Phe	Glu	Asp	Gly	Arg	Glu	Thr	Gln	
	570					575					580					
AGT	AGT	GAA	TCA	ACT	AAT	GAA	TTT	GGG	ATT	TTT	AAT	AGT	CTC	TGG	TTT	1827
Ser	Ser	Glu	Ser	Thr	Asn	Glu	Phe	Gly	Ile	Phe	Asn	Ser	Leu	Trp	Phe	
585					590					595					600	
TCC	TTG	GGT	GCC	TTT	ATG	CGG	CAA	GGA	TGC	GAT	ATT	TCG	CCA	AGA	TCC	1875
Ser	Leu	Gly	Ala	Phe	Met	Arg	Gln	Gly	Cys	Asp	Ile	Ser	Pro	Arg	Ser	
				605					610					615		
CTC	TCT	GGG	CGC	ATT	GTT	GGA	GGT	GTG	TGG	TGG	TTC	TTT	ACC	CTG	ATC	1923
Leu	Ser	Gly	Arg	Ile	Val	Gly	Gly	Val	Trp	Trp	Phe	Phe	Thr	Leu	Ile	
			620					625					630			
ATA	ATC	TCC	TCC	TAC	ACG	GCT	AAC	TTA	GCT	GCC	TTC	CTG	ACT	GTA	GAG	1971
Ile	Ile	Ser	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Thr	Val	Glu	
		635					640					645				
AGG	ATG	GTG	TCT	CCC	ATC	GAA	AGT	GCT	GAG	GAT	CTT	TCT	AAG	CAA	ACA	2019
Arg	Met	Val	Ser	Pro	Ile	Glu	Ser	Ala	Glu	Asp	Leu	Ser	Lys	Gln	Thr	
	650					655					660					
GAA	ATT	GCT	TAT	GGA	ACA	TTA	GAC	TCT	GGC	TCC	ACT	AAA	GAG	TTT	TTC	2067
Glu	Ile	Ala	Tyr	Gly	Thr	Leu	Asp	Ser	Gly	Ser	Thr	Lys	Glu	Phe	Phe	
665					670					675					680	
AGG	AGA	TCT	AAA	ATT	GCA	GTG	TTT	GAT	AAA	ATG	TGG	ACC	TAC	ATG	CGG	2115
Arg	Arg	Ser	Lys	Ile	Ala	Val	Phe	Asp	Lys	Met	Trp	Thr	Tyr	Met	Arg	
				685					690					695		
AGT	GCG	GAG	CCC	TCT	GTG	TTT	GTG	AGG	ACT	ACG	GCC	GAA	GGG	GTG	GCT	2163
Ser	Ala	Glu	Pro	Ser	Val	Phe	Val	Arg	Thr	Thr	Ala	Glu	Gly	Val	Ala	
			700					705					710			
AGA	GTG	CGG	AAG	TCC	AAA	GGG	AAA	TAT	GCC	TAC	TTG	TTG	GAG	TCC	ACG	2211
Arg	Val	Arg	Lys	Ser	Lys	Gly	Lys	Tyr	Ala	Tyr	Leu	Leu	Glu	Ser	Thr	
		715				720					725					
ATG	AAC	GAG	TAC	ATT	GAG	CAA	AGG	AAG	CCT	TGC	GAC	ACC	ATG	AAA	GTT	2259
Met	Asn	Glu	Tyr	Ile	Glu	Gln	Arg	Lys	Pro	Cys	Asp	Thr	Met	Lys	Val	
	730					735					740					
GGT	GGA	AAC	CTG	GAT	TCC	AAA	GGC	TAT	GGC	ATC	GCA	ACA	CCT	AAA	GGA	2307
Gly	Gly	Asn	Leu	Asp	Ser	Lys	Gly	Tyr	Gly	Ile	Ala	Thr	Pro	Lys	Gly	
745					750					755					760	
TCC	TCA	TTA	AGA	AAT	GCG	GTT	AAC	CTC	GCA	GTA	CTA	AAA	CTG	AAT	GAA	2355
Ser	Ser	Leu	Arg	Asn	Ala	Val	Asn	Leu	Ala	Val	Leu	Lys	Leu	Asn	Glu	

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765				770				775								
CAA	GGC	CTG	TTG	GAC	AAA	TTG	AAA	AAC	AAA	TGG	TGG	TAC	GAC	AAA	GGA	2403
Gln	Gly	Leu	Leu	Asp	Lys	Leu	Lys	Asn	Lys	Trp	Trp	Tyr	Asp	Lys	Gly	
			780					785					790			
GAG	TGC	GGC	AGC	GGG	GGA	GGT	GAT	TCC	AAG	GAA	AAG	ACC	AGT	GCC	CTC	2451
Glu	Cys	Gly	Ser	Gly	Gly	Gly	Asp	Ser	Lys	Glu	Lys	Thr	Ser	Ala	Leu	
			795				800						805			
AGT	CTG	AGC	AAC	GTT	GCT	GGA	GTA	TTC	TAC	ATC	CTT	GTC	GGG	GGC	CTT	2499
Ser	Leu	Ser	Asn	Val	Ala	Gly	Val	Phe	Tyr	Ile	Leu	Val	Gly	Gly	Leu	
	810					815						820				
GGT	TTG	GCA	ATG	CTG	GTG	GCT	TTG	ATT	GAG	TTC	TGT	TAC	AAG	TCA	AGG	2547
Gly	Leu	Ala	Met	Leu	Val	Ala	Leu	Ile	Glu	Phe	Cys	Tyr	Lys	Ser	Arg	
					830					835					840	
GCC	GAG	GCG	AAA	CGA	ATG	AAG	GTG	GCA	AAG	AAT	GCA	CAG	AAT	ATT	AAC	2595
Ala	Glu	Ala	Lys	Arg	Met	Lys	Val	Ala	Lys	Asn	Ala	Gln	Asn	Ile	Asn	
				845					850					855		
CCA	TCT	TCC	TCG	CAG	AAT	TCA	CAG	AAT	TTT	GCA	ACT	TAT	AAG	GAA	GGT	2643
Pro	Ser	Ser	Ser	Gln	Asn	Ser	Gln	Asn	Phe	Ala	Thr	Tyr	Lys	Glu	Gly	
			860					865					870			
TAC	AAC	GTA	TAT	GGC	ATC	GAA	AGT	GTT	AAA	ATT	TAGGGGATGA	CCTTGAAATG				2696
Tyr	Asn	Val	Tyr	Gly	Ile	Glu	Ser	Val	Lys	Ile						
		875					880									
ATGCCATGAG	GAACAAGGCA	AGGCTGTCAA	TTACAGGAAG	TACTGGAGAA	AATGGACGTG											2756
TTATGACTCC	AGAATTTCCC	AAAGCAGTGC	ATGCTGTCCC	TTACGTGAGT	CCTGGCATGG											2816
GAATGAATGT	CAGTGTGACT	GATCTCTCGT	GATTGATAAG	AACCTTTTGA	GTGCCTTACA											2876
CAATGGTTTT	CTTGTGTTTA	TTGTCAAAGT	GGTGAGAGGC	ATCCAGTATC	TTGAAGACTT											2936
TTCTTTCAGC	CAAGAATTC															2955

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: protein

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Gln	Lys	Ile	Met	His	Val	Ser	Val	Leu	Leu	Ser	Pro	Val	Leu	Trp
1				5					10					15	
Gly	Leu	Ile	Phe	Gly	Val	Ser	Ser	Asn	Ser	Ile	Gln	Ile	Gly	Gly	Leu
			20					25					30		
Phe	Pro	Arg	Gly	Ala	Asp	Gln	Glu	Tyr	Ser	Ala	Phe	Arg	Val	Gly	Met
		35					40					45			
Val	Gln	Phe	Ser	Thr	Ser	Glu	Phe	Arg	Leu	Thr	Pro	His	Ile	Asp	Asn
	50					55					60				
Leu	Glu	Val	Ala	Asn	Ser	Phe	Ala	Val	Thr	Asn	Ala	Phe	Cys	Ser	Gln
	65				70					75					80
Phe	Ser	Arg	Gly	Val	Tyr	Ala	Ile	Phe	Gly	Phe	Tyr	Asp	Lys	Lys	Ser
				85					90					95	
Val	Asn	Thr	Ile	Thr	Ser	Phe	Cys	Gly	Thr	Leu	His	Val	Ser	Phe	Ile
			100					105					110		
Thr	Pro	Ser	Phe	Pro	Thr	Asp	Gly	Thr	His	Pro	Phe	Val	Ile	Gln	Met
		115					120					125			
Arg	Pro	Asp	Leu	Lys	Gly	Ala	Leu	Leu	Ser	Leu	Ile	Glu	Tyr	Tyr	Gln
	130					135						140			
Trp	Asp	Lys	Phe	Ala	Tyr	Leu	Tyr	Asp	Ser	Asp	Arg	Gly	Leu	Ser	Thr

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145				150				155				160			
Leu	Gln	Ala	Val	Leu 165	Asp	Ser	Ala	Ala	Glu 170	Lys	Lys	Trp	Gln	Val 175	Thr
Ala	Ile	Asn	Val 180	Gly	Asn	Ile	Asn 185	Asn	Asp	Lys	Lys	Asp	Glu 190	Met	Tyr
Arg	Ser	Leu 195	Phe	Gln	Asp	Leu	Glu 200	Leu	Lys	Lys	Glu	Arg 205	Arg	Val	Ile
Leu	Asp 210	Cys	Glu	Arg	Asp	Lys 215	Val	Asn	Asp	Ile	Val 220	Asp	Gln	Val	Ile
Thr 225	Ile	Gly	Lys	His	Val 230	Lys	Gly	Tyr	His	Tyr 235	Ile	Ile	Ala	Asn	Leu 240
Gly	Phe	Thr	Asp	Gly 245	Asp	Leu	Leu	Lys	Ile 250	Gln	Phe	Gly	Gly	Ala 255	Asn
Val	Ser	Gly	Phe 260	Gln	Ile	Val	Asp	Tyr 265	Asp	Asp	Ser	Leu	Val 270	Ser	Lys
Phe	Ile	Glu 275	Arg	Trp	Ser	Thr	Leu 280	Glu	Glu	Lys	Glu	Tyr 285	Pro	Gly	Ala
His	Thr 290	Thr	Thr	Ile	Lys	Tyr 295	Thr	Ser	Ala	Leu	Thr 300	Tyr	Asp	Ala	Val
Gln 305	Val	Met	Thr	Glu	Ala 310	Phe	Arg	Asn	Leu	Arg 315	Lys	Gln	Arg	Ile	Glu 320
Ile	Ser	Arg	Arg	Gly 325	Asn	Ala	Gly	Asp	Cys 330	Leu	Ala	Asn	Pro	Ala	Val 335
Pro	Trp	Gly	Gln 340	Gly	Val	Glu	Ile	Glu 345	Arg	Ala	Leu	Lys	Gln 350	Val	Gln
Val	Glu	Gly 355	Leu	Ser	Gly	Asn	Ile 360	Lys	Phe	Asp	Gln 365	Asn	Gly	Lys	Arg
Ile 370	Asn	Tyr	Thr	Ile	Asn	Ile 375	Met	Glu	Leu	Lys	Thr 380	Asn	Gly	Pro	Arg
Lys 385	Ile	Gly	Tyr	Trp	Ser	Glu 390	Val	Asp	Lys	Met 395	Val	Val	Thr	Leu	Thr 400
Glu	Leu	Pro	Ser	Gly 405	Asn	Asp	Thr	Ser	Gly 410	Leu	Glu	Asn	Lys	Thr 415	Val
Val	Val	Thr	Thr 420	Ile	Leu	Glu	Ser	Pro 425	Tyr	Val	Met	Met	Lys 430	Lys	Asn
His	Glu	Met 435	Leu	Glu	Gly	Asn	Glu 440	Arg	Tyr	Glu	Gly	Tyr 445	Cys	Val	Asp
Leu	Ala	Ala	Glu	Ile	Ala	Lys 455	His	Cys	Gly	Phe	Lys 460	Tyr	Lys	Leu	Thr
Ile 465	Val	Gly	Asp	Gly	Lys 470	Tyr	Gly	Ala	Arg	Asp 475	Ala	Asp	Thr	Lys	Ile 480
Trp	Asn	Gly	Met 485	Val	Gly	Glu	Leu	Val	Tyr 490	Gly	Lys	Ala	Asp	Ile 495	Ala
Ile	Ala	Pro	Leu 500	Thr	Ile	Thr	Leu	Val 505	Arg	Glu	Glu	Val 510	Ile	Asp	Phe
Ser	Lys	Pro 515	Phe	Met	Ser	Leu	Gly 520	Ile	Ser	Ile	Met	Ile 525	Lys	Lys	Pro
Gln	Lys 530	Ser	Lys	Pro	Gly	Val 535	Phe	Ser	Phe	Leu	Asp 540	Pro	Leu	Ala	Tyr
Glu 545	Ile	Trp	Met	Cys	Ile 550	Val	Phe	Ala	Tyr	Ile 555	Gly	Val	Ser	Val	Val 560
Leu	Phe	Leu	Val	Ser 565	Arg	Phe	Ser	Pro	Tyr 570	Glu	Trp	His	Thr	Glu	Glu 575

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Phe	Glu	Asp	Gly	Arg	Glu	Thr	Gln	Ser	Ser	Glu	Ser	Thr	Asn	Glu	Phe
			580					585					590		
Gly	Ile	Phe	Asn	Ser	Leu	Trp	Phe	Ser	Leu	Gly	Ala	Phe	Met	Arg	Gln
		595					600					605			
Gly	Cys	Asp	Ile	Ser	Pro	Arg	Ser	Leu	Ser	Gly	Arg	Ile	Val	Gly	Gly
	610					615					620				
Val	Trp	Trp	Phe	Phe	Thr	Leu	Ile	Ile	Ile	Ser	Ser	Tyr	Thr	Ala	Asn
625					630					635					640
Leu	Ala	Ala	Phe	Leu	Thr	Val	Glu	Arg	Met	Val	Ser	Pro	Ile	Glu	Ser
			645						650					655	
Ala	Glu	Asp	Leu	Ser	Lys	Gln	Thr	Glu	Ile	Ala	Tyr	Gly	Thr	Leu	Asp
			660					665					670		
Ser	Gly	Ser	Thr	Lys	Glu	Phe	Phe	Arg	Arg	Ser	Lys	Ile	Ala	Val	Phe
		675					680					685			
Asp	Lys	Met	Trp	Thr	Tyr	Met	Arg	Ser	Ala	Glu	Pro	Ser	Val	Phe	Val
	690					695					700				
Arg	Thr	Thr	Ala	Glu	Gly	Val	Ala	Arg	Val	Arg	Lys	Ser	Lys	Gly	Lys
705					710					715					720
Tyr	Ala	Tyr	Leu	Leu	Glu	Ser	Thr	Met	Asn	Glu	Tyr	Ile	Glu	Gln	Arg
			725						730					735	
Lys	Pro	Cys	Asp	Thr	Met	Lys	Val	Gly	Gly	Asn	Leu	Asp	Ser	Lys	Gly
			740					745					750		
Tyr	Gly	Ile	Ala	Thr	Pro	Lys	Gly	Ser	Ser	Leu	Arg	Asn	Ala	Val	Asn
	755						760					765			
Leu	Ala	Val	Leu	Lys	Leu	Asn	Glu	Gln	Gly	Leu	Leu	Asp	Lys	Leu	Lys
	770					775					780				
Asn	Lys	Trp	Trp	Tyr	Asp	Lys	Gly	Glu	Cys	Gly	Ser	Gly	Gly	Gly	Asp
785					790					795					800
Ser	Lys	Glu	Lys	Thr	Ser	Ala	Leu	Ser	Leu	Ser	Asn	Val	Ala	Gly	Val
				805					810					815	
Phe	Tyr	Ile	Leu	Val	Gly	Gly	Leu	Gly	Leu	Ala	Met	Leu	Val	Ala	Leu
			820					825					830		
Ile	Glu	Phe	Cys	Tyr	Lys	Ser	Arg	Ala	Glu	Ala	Lys	Arg	Met	Lys	Val
		835					840					845			
Ala	Lys	Asn	Ala	Gln	Asn	Ile	Asn	Pro	Ser	Ser	Ser	Gln	Asn	Ser	Gln
	850					855					860				
Asn	Phe	Ala	Thr	Tyr	Lys	Glu	Gly	Tyr	Asn	Val	Tyr	Gly	Ile	Glu	Ser
865					870					875					880
Val	Lys	Ile													

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA to mRNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) DEVELOPMENTAL STAGE: adult
- (C) TISSUE TYPE: brain

(i x) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 73..2736

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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CTGACGACTC	CTGAGTTGCG	CCCATGCTCT	TGTCAGCTTC	GTTTTAGGCG	TAGCATGGCC												60
AGGCAGAAGA	AA	ATG	GGG	CAA	AGC	GTG	CTC	CGG	GCG	GTC	TTC	TTT	TTA				108
		Met	Gly	Gln	Ser	Val	Leu	Arg	Ala	Val	Phe	Phe	Leu				
		1					5					10					
GTC	CTG	GGG	CTT	TTG	GGT	CAT	TCT	CAC	GGA	GGA	TTC	CCC	AAC	ACC	ATC		156
Val	Leu	Gly	Leu	Leu	Gly	His	Ser	His	Gly	Gly	Phe	Pro	Asn	Thr	Ile		
		15					20					25					
AGC	ATA	GGT	GGA	CTT	TTC	ATG	AGA	AAC	ACA	GTG	CAG	GAG	CAC	AGC	GCT		204
Ser	Ile	Gly	Gly	Leu	Phe	Met	Arg	Asn	Thr	Val	Gln	Glu	His	Ser	Ala		
	30					35				40							
TTC	CGC	TTT	GCC	GTG	CAG	TTA	TAC	AAC	ACC	AAC	CAG	AAC	ACC	ACC	GAG		252
Phe	Arg	Phe	Ala	Val	Gln	Leu	Tyr	Asn	Thr	Asn	Gln	Asn	Thr	Thr	Glu		
	45				50					55					60		
AAG	CCC	TTC	CAT	TTG	AAT	TAC	CAC	GTA	GAT	CAC	TTG	GAT	TCC	TCC	AAT		300
Lys	Pro	Phe	His	Leu	Asn	Tyr	His	Val	Asp	His	Leu	Asp	Ser	Ser	Asn		
				65					70					75			
AGT	TTT	TCC	GTG	ACA	AAT	GCT	TTC	TGC	TCC	CAG	TTC	TCG	AGA	GGG	GTG		348
Ser	Phe	Ser	Val	Thr	Asn	Ala	Phe	Cys	Ser	Gln	Phe	Ser	Arg	Gly	Val		
			80					85					90				
TAT	GCC	ATC	TTT	GGA	TTC	TAT	GAC	CAG	ATG	TCA	ATG	AAC	ACC	CTG	ACC		396
Tyr	Ala	Ile	Phe	Gly	Phe	Tyr	Asp	Gln	Met	Ser	Met	Asn	Thr	Leu	Thr		
		95					100					105					
TCC	TTC	TGT	GGG	GCC	CTG	CAC	ACA	TCC	TTT	GTT	ACG	CCT	AGC	TTC	CCC		444
Ser	Phe	Cys	Gly	Ala	Leu	His	Thr	Ser	Phe	Val	Thr	Pro	Ser	Phe	Pro		
	110					115					120						
ACT	GAC	GCA	GAT	GTG	CAG	TTT	GTC	ATC	CAG	ATG	CGC	CCA	GCC	TTG	AAG		492
Thr	Asp	Ala	Asp	Val	Gln	Phe	Val	Ile	Gln	Met	Arg	Pro	Ala	Leu	Lys		
	125				130					135					140		
GGC	GCT	ATT	CTG	AGT	CTT	CTG	GGT	CAT	TAC	AAG	TGG	GAG	AAG	TTT	GTG		540
Gly	Ala	Ile	Leu	Ser	Leu	Leu	Gly	His	Tyr	Lys	Trp	Glu	Lys	Phe	Val		
				145					150					155			
TAC	CTC	TAT	GAC	ACA	GAA	CGA	GGA	TTT	TCC	ATC	CTC	CAA	GCG	ATT	ATG		588
Tyr	Leu	Tyr	Asp	Thr	Glu	Arg	Gly	Phe	Ser	Ile	Leu	Gln	Ala	Ile	Met		
			160					165					170				
GAA	GCA	GCA	GTG	CAA	AAC	AAC	TGG	CAA	GTA	ACA	GCA	AGG	TCT	GTG	GGA		636
Glu	Ala	Ala	Val	Gln	Asn	Asn	Trp	Gln	Val	Thr	Ala	Arg	Ser	Val	Gly		
		175					180					185					
AAC	ATA	AAG	GAC	GTC	CAA	GAA	TTC	AGG	CGC	ATC	ATT	GAA	GAA	ATG	GAC		684
Asn	Ile	Lys	Asp	Val	Gln	Glu	Phe	Arg	Arg	Ile	Ile	Glu	Glu	Met	Asp		
	190					195					200						
AGG	AGG	CAG	GAA	AAG	CGA	TAC	TTG	ATT	GAC	TGC	GAA	GTC	GAA	AGG	ATT		732
Arg	Arg	Gln	Glu	Lys	Arg	Tyr	Leu	Ile	Asp	Cys	Glu	Val	Glu	Arg	Ile		
	205				210					215					220		
AAC	ACA	ATT	TTG	GAA	CAG	GTT	GTG	ATC	CTA	GGG	AAA	CAC	TCA	AGA	GGT		780
Asn	Thr	Ile	Leu	Glu	Gln	Val	Val	Ile	Leu	Gly	Lys	His	Ser	Arg	Gly		
				225					230					235			
TAT	CAC	TAC	ATG	CTC	GCT	AAC	CTG	GGT	TTT	ACT	GAT	ATT	TTA	CTG	GAA		828
Tyr	His	Tyr	Met	Leu	Ala	Asn	Leu	Gly	Phe	Thr	Asp	Ile	Leu	Leu	Glu		
			240					245					250				
AGA	GTC	ATG	CAT	GGG	GGA	GCC	AAC	ATT	ACA	GGT	TTC	CAG	ATT	GTC	AAC		876
Arg	Val	Met	His	Gly	Gly	Ala	Asn	Ile	Thr	Gly	Phe	Gln	Ile	Val	Asn		
		255					260					265					
AAT	GAA	AAC	CCT	ATG	GTT	CAG	CAG	TTC	ATA	CAG	CGC	TGG	GTG	AGG	CTG		924
Asn	Glu	Asn	Pro	Met	Val	Gln	Gln	Phe	Ile	Gln	Arg	Trp	Val	Arg	Leu		
	270					275					280						
GAT	GAA	AGG	GAA	TTC	CCT	GAA	GCC	AAG	AAT	GCA	CCA	CTA	AAG	TAT	ACA		972
Asp	Glu	Arg	Glu	Phe	Pro	Glu	Ala	Lys	Asn	Ala	Pro	Leu	Lys	Tyr	Thr		
					290					295					300		
TCT	GCA	TTG	ACA	CAC	GAC	GCA	ATA	CTG	GTC	ATA	GCA	GAA	GCT	TTC	CGC		1020

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Ser	Ala	Leu	Thr	His	Asp	Ala	Ile	Leu	Val	Ile	Ala	Glu	Ala	Phe	Arg	
				305					310					315		
TAC	CTG	AGG	AGG	CAG	CGA	GTA	GAT	GTG	TCC	CGG	AGA	GGA	AGT	GCT	GGA	1068
Tyr	Leu	Arg	Arg	Gln	Arg	Val	Asp	Val	Ser	Arg	Arg	Gly	Ser	Ala	Gly	
			320					325					330			
GAC	TGC	TTA	GCA	AAT	CCT	GCT	GTG	CCC	TGG	AGT	CAA	GGA	ATT	GAT	ATT	1116
Asp	Cys	Leu	Ala	Asn	Pro	Ala	Val	Pro	Trp	Ser	Gln	Gly	Ile	Asp	Ile	
		335					340					345				
GAG	AGA	GCT	CTG	AAA	ATG	GTG	CAA	GTA	CAA	GGA	ATG	ACT	GGA	AAT	ATT	1164
Glu	Arg	Ala	Leu	Lys	Met	Val	Gln	Val	Gln	Gly	Met	Thr	Gly	Asn	Ile	
	350					355					360					
CAA	TTT	GAC	ACT	TAT	GGA	CGT	AGG	ACA	AAT	TAT	ACC	ATC	GAT	GTG	TAT	1212
Gln	Phe	Asp	Thr	Tyr	Gly	Arg	Arg	Thr	Asn	Tyr	Thr	Ile	Asp	Val	Tyr	
365					370					375					380	
GAA	ATG	AAA	GTC	AGT	GGC	TCT	CGA	AAA	GCT	GGC	TAC	TGG	AAC	GAG	TAT	1260
Glu	Met	Lys	Val	Ser	Gly	Ser	Arg	Lys	Ala	Gly	Tyr	Trp	Asn	Glu	Tyr	
				385				390						395		
GAA	AGG	TTT	GTG	CCT	TTC	TCA	GAT	CAG	CAA	ATC	AGC	AAT	GAC	AGT	GCA	1308
Glu	Arg	Phe	Val	Pro	Phe	Ser	Asp	Gln	Gln	Ile	Ser	Asn	Asp	Ser	Ala	
			400					405					410			
TCC	TCA	GAG	AAT	CGG	ACC	ATA	GTA	GTG	ACT	ACC	ATT	CTG	GAA	TCA	CCA	1356
Ser	Ser	Glu	Asn	Arg	Thr	Ile	Val	Val	Thr	Thr	Ile	Leu	Glu	Ser	Pro	
		415					420					425				
TAT	GTA	ATG	TAC	AAG	AAG	AAC	CAT	GAG	CAA	CTG	GAA	GGA	AAT	GAA	CGA	1404
Tyr	Val	Met	Tyr	Lys	Lys	Asn	His	Glu	Gln	Leu	Glu	Gly	Asn	Glu	Arg	
	430					435					440					
TAT	GAA	GGC	TAT	TGT	GTA	GAC	CTA	GCC	TAT	GAA	ATA	GCC	AAA	CAT	GTA	1452
Tyr	Glu	Gly	Tyr	Cys	Val	Asp	Leu	Ala	Tyr	Glu	Ile	Ala	Lys	His	Val	
	445			450						455					460	
AGG	ATC	AAA	TAC	AAA	TTG	TCC	ATC	GTT	GGT	GAC	GGG	AAA	TAT	GGT	GCA	1500
Arg	Ile	Lys	Tyr	Lys	Leu	Ser	Ile	Val	Gly	Asp	Gly	Lys	Tyr	Gly	Ala	
				465				470						475		
AGG	GAT	CCA	GAG	ACT	AAA	ATA	TGG	AAC	GGC	ATG	GTT	GGG	GAA	CTT	GTC	1548
Arg	Asp	Pro	Glu	Thr	Lys	Ile	Trp	Asn	Gly	Met	Val	Gly	Glu	Leu	Val	
			480					485					490			
TAT	GGG	AGA	GCT	GAT	ATA	GCT	GTT	GCT	CCA	CTC	ACT	ATA	ACA	TTG	GTC	1596
Tyr	Gly	Arg	Ala	Asp	Ile	Ala	Val	Ala	Pro	Leu	Thr	Ile	Thr	Leu	Val	
		495					500					505				
CGT	GAA	GAA	GTC	ATA	GAT	TTT	TCA	AAG	CCA	TTC	ATG	AGC	CTG	GGC	ATC	1644
Arg	Glu	Glu	Val	Ile	Asp	Phe	Ser	Lys	Pro	Phe	Met	Ser	Leu	Gly	Ile	
	510					515					520					
TCC	ATC	ATG	ATA	AAG	AAG	CCT	CAG	AAA	TCA	AAA	CCA	GGC	GTA	TTC	TCA	1692
Ser	Ile	Met	Ile	Lys	Lys	Pro	Gln	Lys	Ser	Lys	Pro	Gly	Val	Phe	Ser	
					530					535					540	
TTT	CTG	GAT	CCC	CTG	GCT	TAT	GAA	ATC	TGG	ATG	TGC	ATT	GTC	TTT	GCT	1740
Phe	Leu	Asp	Pro	Leu	Ala	Tyr	Glu	Ile	Trp	Met	Cys	Ile	Val	Phe	Ala	
				545					550					555		
TAC	ATT	GGA	GTC	AGC	GTA	GTT	CTT	TTC	CTA	GTC	AGC	AGG	TTC	AGT	CCT	1788
Tyr	Ile	Gly	Val	Ser	Val	Val	Leu	Phe	Leu	Val	Ser	Arg	Phe	Ser	Pro	
			560					565					570			
TAT	GAA	TGG	CAC	TTG	GAA	GAC	AAC	AAT	GAA	GAA	CCT	CGT	GAC	CCA	CAA	1836
Tyr	Glu	Trp	His	Leu	Glu	Asp	Asn	Asn	Glu	Glu	Pro	Arg	Asp	Pro	Gln	
		575					580					585				
AGT	CCT	CCT	GAT	CCT	CCA	AAT	GAA	TTT	GGA	ATA	TTT	AAC	AGT	CTT	TGG	1884
Ser	Pro	Pro	Asp	Pro	Pro	Asn	Glu	Phe	Gly	Ile	Phe	Asn	Ser	Leu	Trp	
	590					595					600					
TTT	TCC	TTG	GGT	GCC	TTT	ATG	CAG	CAA	GGA	TGT	GAT	ATT	TCT	CCA	AGA	1932
Phe	Ser	Leu	Gly	Ala	Phe	Met	Gln	Gln	Gly	Cys	Asp	Ile	Ser	Pro	Arg	
	605				610					615					620	
TCA	CTC	TCC	GGG	CGC	ATT	GTT	GGA	GGG	GTT	TGG	TGG	TTC	TTC	ACC	CTG	1980

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Ser	Leu	Ser	Gly	Arg	Ile	Val	Gly	Gly	Val	Trp	Trp	Phe	Phe	Thr	Leu	
				625					630					635		
ATC	ATA	ATT	TCT	TCC	TAT	ACT	GCC	AAT	CTC	GCT	GCT	TTC	CTG	ACT	GTG	2028
Ile	Ile	Ile	Ser	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Thr	Val	
			640					645					650			
GAG	AGG	ATG	GTT	TCT	CCC	ATA	GAG	AGT	GCT	GAA	GAC	TTA	GCT	AAA	CAG	2076
Glu	Arg	Met	Val	Ser	Pro	Ile	Glu	Ser	Ala	Glu	Asp	Leu	Ala	Lys	Gln	
		655					660					665				
ACT	GAA	ATT	GCA	TAT	GGG	ACC	CTG	GAC	TCC	GGT	TCA	ACA	AAA	GAA	TTT	2124
Thr	Glu	Ile	Ala	Tyr	Gly	Thr	Leu	Asp	Ser	Gly	Ser	Thr	Lys	Glu	Phe	
	670					675					680					
TTC	AGA	AGA	TCC	AAA	ATT	GCT	GTG	TAC	GAG	AAA	ATG	TGG	TCT	TAC	ATG	2172
Phe	Arg	Arg	Ser	Lys	Ile	Ala	Val	Tyr	Glu	Lys	Met	Trp	Ser	Tyr	Met	
					690					695					700	
AAA	TCA	GCG	GAG	CCA	TCT	GTG	TTT	ACC	AAA	ACA	ACA	GCA	GAC	GGA	GTG	2220
Lys	Ser	Ala	Glu	Pro	Ser	Val	Phe	Thr	Lys	Thr	Thr	Ala	Asp	Gly	Val	
				705					710					715		
GCC	CGA	GTG	CGA	AAG	TCC	AAG	GGA	AAG	TTC	GCC	TTC	CTG	CTG	GAG	TCA	2268
Ala	Arg	Val	Arg	Lys	Ser	Lys	Gly	Lys	Phe	Ala	Phe	Leu	Leu	Glu	Ser	
			720					725					730			
ACC	ATG	AAT	GAG	TAC	ATT	GAG	CAG	AGA	AAA	CCA	TGT	GAT	ACG	ATG	AAA	2316
Thr	Met	Asn	Glu	Tyr	Ile	Glu	Gln	Arg	Lys	Pro	Cys	Asp	Thr	Met	Lys	
		735					740					745				
GTT	GGT	GGA	AAT	CTG	GAT	TCC	AAA	GGC	TAT	GGT	GTG	GCA	ACC	CCT	AAA	2364
Val	Gly	Gly	Asn	Leu	Asp	Ser	Lys	Gly	Tyr	Gly	Val	Ala	Thr	Pro	Lys	
	750					755					760					
GGC	TCA	GCA	TTA	GGA	ACG	CCT	GTA	AAC	CTT	GCA	GTA	TTG	AAA	CTC	AGT	2412
Gly	Ser	Ala	Leu	Gly	Thr	Pro	Val	Asn	Leu	Ala	Val	Leu	Lys	Leu	Ser	
				770					775						780	
GAA	CAA	GGC	ATC	TTA	GAC	AAG	CTG	AAA	AAC	AAA	TGG	TGG	TAC	GAT	AAG	2460
Glu	Gln	Gly	Ile	Leu	Asp	Lys	Leu	Lys	Asn	Lys	Trp	Trp	Tyr	Asp	Lys	
				785					790					795		
GGG	GAA	TGT	GGA	GCC	AAG	GAC	TCC	GGG	AGT	AAG	GAC	AAG	ACC	AGC	GCT	2508
Gly	Glu	Cys	Gly	Ala	Lys	Asp	Ser	Gly	Ser	Lys	Asp	Lys	Thr	Ser	Ala	
			800					805					810			
CTG	AGC	CTG	AGC	AAT	GTG	GCA	GGC	GTT	TTC	TAT	ATA	CTT	GTC	GGA	GGT	2556
Leu	Ser	Leu	Ser	Asn	Val	Ala	Gly	Val	Phe	Tyr	Ile	Leu	Val	Gly	Gly	
		815					820					825				
CTG	GGG	CTG	GCC	ATG	ATG	GTG	GCT	TTG	ATA	GAA	TTC	TGT	TAC	AAA	TCA	2604
Leu	Gly	Leu	Ala	Met	Met	Val	Ala	Leu	Ile	Glu	Phe	Cys	Tyr	Lys	Ser	
	830					835					840					
CGG	GCA	GAG	TCC	AAA	CGC	ATG	AAA	CTC	ACA	AAG	AAC	ACC	CAA	AAC	TTT	2652
Arg	Ala	Glu	Ser	Lys	Arg	Met	Lys	Leu	Thr	Lys	Asn	Thr	Gln	Asn	Phe	
					850					855					860	
AAG	CCT	GCT	CCT	GCC	ACC	AAC	ACT	CAG	AAT	TAT	GCT	ACA	TAC	AGA	GAA	2700
Lys	Pro	Ala	Pro	Ala	Thr	Asn	Thr	Gln	Asn	Tyr	Ala	Thr	Tyr	Arg	Glu	
				865					870					875		
GGC	TAC	AAC	GTG	TAT	GGA	ACA	GAG	AGT	GTT	AAG	ATC	TAGGGATCCC				2746
Gly	Tyr	Asn	Val	Tyr	Gly	Thr	Glu	Ser	Val	Lys	Ile					
			880					885								
TTCCCACTGG AGGCATGTGA TGAGAGGAAA TCACCGAAAA CGTGGCTGCT TCAAGGATCC															2806	
TGAGCCAGAT TTCACTCTCC TTGGTGTCCG GCATGACACG AATATTGCTG ATGGTGCAAT															2866	
GACCTTTCAA TAGGAAAAAC TGGTTTTTTT TTCCTTCAGT GCCTTATGGA ACACTCTGAG															2926	
ACTCGCGACA ATGCAAACCA TCATTGAAAT CTTTTTGCTT TGCTTGAAAA AAAAAAAAAA															2986	
AAA															2989	

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: protein

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Gly	Gln	Ser	Val	Leu	Arg	Ala	Val	Phe	Phe	Leu	Val	Leu	Gly	Leu	1	5	10	15
Leu	Gly	His	Ser	His	Gly	Gly	Phe	Pro	Asn	Thr	Ile	Ser	Ile	Gly	Gly	20	25	30	
Leu	Phe	Met	Arg	Asn	Thr	Val	Gln	Glu	His	Ser	Ala	Phe	Arg	Phe	Ala	35	40	45	
Val	Gln	Leu	Tyr	Asn	Thr	Asn	Gln	Asn	Thr	Thr	Glu	Lys	Pro	Phe	His	50	55	60	
Leu	Asn	Tyr	His	Val	Asp	His	Leu	Asp	Ser	Ser	Asn	Ser	Phe	Ser	Val	65	70	75	80
Thr	Asn	Ala	Phe	Cys	Ser	Gln	Phe	Ser	Arg	Gly	Val	Tyr	Ala	Ile	Phe	85	90	95	
Gly	Phe	Tyr	Asp	Gln	Met	Ser	Met	Asn	Thr	Leu	Thr	Ser	Phe	Cys	Gly	100	105	110	
Ala	Leu	His	Thr	Ser	Phe	Val	Thr	Pro	Ser	Phe	Pro	Thr	Asp	Ala	Asp	115	120	125	
Val	Gln	Phe	Val	Ile	Gln	Met	Arg	Pro	Ala	Leu	Lys	Gly	Ala	Ile	Leu	130	135	140	
Ser	Leu	Leu	Gly	His	Tyr	Lys	Trp	Glu	Lys	Phe	Val	Tyr	Leu	Tyr	Asp	145	150	155	160
Thr	Glu	Arg	Gly	Phe	Ser	Ile	Leu	Gln	Ala	Ile	Met	Glu	Ala	Ala	Val	165	170	175	
Gln	Asn	Asn	Trp	Gln	Val	Thr	Ala	Arg	Ser	Val	Gly	Asn	Ile	Lys	Asp	180	185	190	
Val	Gln	Glu	Phe	Arg	Arg	Ile	Ile	Glu	Glu	Met	Asp	Arg	Arg	Gln	Glu	195	200	205	
Lys	Arg	Tyr	Leu	Ile	Asp	Cys	Glu	Val	Glu	Arg	Ile	Asn	Thr	Ile	Leu	210	215	220	
Glu	Gln	Val	Val	Ile	Leu	Gly	Lys	His	Ser	Arg	Gly	Tyr	His	Tyr	Met	225	230	235	240
Leu	Ala	Asn	Leu	Gly	Phe	Thr	Asp	Ile	Leu	Leu	Glu	Arg	Val	Met	His	245	250	255	
Gly	Gly	Ala	Asn	Ile	Thr	Gly	Phe	Gln	Ile	Val	Asn	Asn	Glu	Asn	Pro	260	265	270	
Met	Val	Gln	Gln	Phe	Ile	Gln	Arg	Trp	Val	Arg	Leu	Asp	Glu	Arg	Glu	275	280	285	
Phe	Pro	Glu	Ala	Lys	Asn	Ala	Pro	Leu	Lys	Tyr	Thr	Ser	Ala	Leu	Thr	290	295	300	
His	Asp	Ala	Ile	Leu	Val	Ile	Ala	Glu	Ala	Phe	Arg	Tyr	Leu	Arg	Arg	305	310	315	320
Gln	Arg	Val	Asp	Val	Ser	Arg	Arg	Gly	Ser	Ala	Gly	Asp	Cys	Leu	Ala	325	330	335	
Asn	Pro	Ala	Val	Pro	Trp	Ser	Gln	Gly	Ile	Asp	Ile	Glu	Arg	Ala	Leu	340	345	350	
Lys	Met	Val	Gln	Val	Gln	Gly	Met	Thr	Gly	Asn	Ile	Gln	Phe	Asp	Thr	355	360	365	
Tyr	Gly	Arg	Arg	Thr	Asn	Tyr	Thr	Ile	Asp	Val	Tyr	Glu	Met	Lys	Val	370	375	380	

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Ser 385	Gly	Ser	Arg	Lys	Ala 390	Gly	Tyr	Trp	Asn	Glu 395	Tyr	Glu	Arg	Phe	Val 400
Pro	Phe	Ser	Asp	Gln 405	Gln	Ile	Ser	Asn	Asp 410	Ser	Ala	Ser	Ser	Glu 415	Asn
Arg	Thr	Ile	Val 420	Val	Thr	Thr	Ile	Leu 425	Glu	Ser	Pro	Tyr	Val 430	Met	Tyr
Lys	Lys	Asn 435	His	Glu	Gln	Leu	Glu 440	Gly	Asn	Glu	Arg	Tyr 445	Glu	Gly	Tyr
Cys	Val 450	Asp	Leu	Ala	Tyr	Glu 455	Ile	Ala	Lys	His	Val 460	Arg	Ile	Lys	Tyr
Lys 465	Leu	Ser	Ile	Val	Gly 470	Asp	Gly	Lys	Tyr	Gly 475	Ala	Arg	Asp	Pro	Glu 480
Thr	Lys	Ile	Trp	Asn 485	Gly	Met	Val	Gly	Glu 490	Leu	Val	Tyr	Gly	Arg 495	Ala
Asp	Ile	Ala	Val 500	Ala	Pro	Leu	Thr	Ile 505	Thr	Leu	Val	Arg	Glu 510	Glu	Val
Ile	Asp	Phe 515	Ser	Lys	Pro	Phe	Met 520	Ser	Leu	Gly	Ile	Ser 525	Ile	Met	Ile
Lys 530	Lys	Pro	Gln	Lys	Ser	Lys 535	Pro	Gly	Val	Phe	Ser 540	Phe	Leu	Asp	Pro
Leu 545	Ala	Tyr	Glu	Ile	Trp 550	Met	Cys	Ile	Val	Phe 555	Ala	Tyr	Ile	Gly	Val 560
Ser	Val	Val	Leu	Phe 565	Leu	Val	Ser	Arg	Phe 570	Ser	Pro	Tyr	Glu	Trp 575	His
Leu	Glu	Asp	Asn 580	Asn	Glu	Glu	Pro	Arg 585	Asp	Pro	Gln	Ser	Pro 590	Pro	Asp
Pro	Pro	Asn 595	Glu	Phe	Gly	Ile	Phe 600	Asn	Ser	Leu	Trp	Phe 605	Ser	Leu	Gly
Ala 610	Phe	Met	Gln	Gln	Gly	Cys 615	Asp	Ile	Ser	Pro	Arg 620	Ser	Leu	Ser	Gly
Arg 625	Ile	Val	Gly	Gly	Val 630	Trp	Trp	Phe	Phe	Thr 635	Leu	Ile	Ile	Ile	Ser 640
Ser	Tyr	Thr	Ala	Asn 645	Leu	Ala	Ala	Phe	Leu 650	Thr	Val	Glu	Arg	Met 655	Val
Ser	Pro	Ile	Glu 660	Ser	Ala	Glu	Asp	Leu 665	Ala	Lys	Gln	Thr	Glu 670	Ile	Ala
Tyr	Gly	Thr 675	Leu	Asp	Ser	Gly	Ser 680	Thr	Lys	Glu	Phe	Phe 685	Arg	Arg	Ser
Lys 690	Ile	Ala	Val	Tyr	Glu	Lys 695	Met	Trp	Ser	Tyr	Met 700	Lys	Ser	Ala	Glu
Pro 705	Ser	Val	Phe	Thr	Lys 710	Thr	Thr	Ala	Asp	Gly 715	Val	Ala	Arg	Val	Arg 720
Lys	Ser	Lys	Gly	Lys 725	Phe	Ala	Phe	Leu 730	Leu	Glu	Ser	Thr	Met	Asn 735	Glu
Tyr	Ile	Glu	Gln 740	Arg	Lys	Pro	Cys	Asp 745	Thr	Met	Lys	Val	Gly 750	Gly	Asn
Leu	Asp	Ser 755	Lys	Gly	Tyr	Gly	Val 760	Ala	Thr	Pro	Lys	Gly 765	Ser	Ala	Leu
Gly 770	Thr	Pro	Val	Asn	Leu	Ala 775	Val	Leu	Lys	Leu	Ser 780	Glu	Gln	Gly	Ile
Leu 785	Asp	Lys	Leu	Lys	Asn 790	Lys	Trp	Trp	Tyr	Asp 795	Lys	Gly	Glu	Cys	Gly 800
Ala	Lys	Asp	Ser	Gly	Ser	Lys	Asp	Lys	Thr	Ser	Ala	Leu	Ser	Leu	Ser

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805				810				815							
Asn	Val	Ala	Gly	Val	Phe	Tyr	Ile	Leu	Val	Gly	Gly	Leu	Gly	Leu	Ala
			820					825				830			
Met	Met	Val	Ala	Leu	Ile	Glu	Phe	Cys	Tyr	Lys	Ser	Arg	Ala	Glu	Ser
		835					840					845			
Lys	Arg	Met	Lys	Leu	Thr	Lys	Asn	Thr	Gln	Asn	Phe	Lys	Pro	Ala	Pro
	850					855					860				
Ala	Thr	Asn	Thr	Gln	Asn	Tyr	Ala	Thr	Tyr	Arg	Glu	Gly	Tyr	Asn	Val
865					870					875					880
Tyr	Gly	Thr	Glu	Ser	Val	Lys	Ile								
				885											

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA to mRNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) DEVELOPMENTAL STAGE: adult
- (C) TISSUE TYPE: brain

(i x) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 73..2736

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTGACGACTC	CTGAGTTGCG	CCCATGCTCT	TGTCAGCTTC	GTTTTAGGCG	TAGCATGGCC												60
AGGCAGAAGA	AA	ATG	GGG	CAA	AGC	GTG	CTC	CGG	GCG	GTC	TTC	TTT	TTA				108
		Met	Gly	Gln	Ser	Val	Leu	Arg	Ala	Val	Phe	Phe	Leu				
		1				5						10					
GTC	CTG	GGG	CTT	TTG	GGT	CAT	TCT	CAC	GGA	GGA	TTC	CCC	AAC	ACC	ATC		156
Val	Leu	Gly	Leu	Leu	Gly	His	Ser	His	Gly	Gly	Phe	Pro	Asn	Thr	Ile		
		15				20						25					
AGC	ATA	GGT	GGA	CTT	TTC	ATG	AGA	AAC	ACA	GTG	CAG	GAG	CAC	AGC	GCT		204
Ser	Ile	Gly	Gly	Leu	Phe	Met	Arg	Asn	Thr	Val	Gln	Glu	His	Ser	Ala		
	30					35					40						
TTC	CGC	TTT	GCC	GTG	CAG	TTA	TAC	AAC	ACC	AAC	CAG	AAC	ACC	ACC	GAG		252
Phe	Arg	Phe	Ala	Val	Gln	Leu	Tyr	Asn	Thr	Asn	Gln	Asn	Thr	Thr	Glu		
	45				50					55					60		
AAG	CCC	TTC	CAT	TTG	AAT	TAC	CAC	GTA	GAT	CAC	TTG	GAT	TCC	TCC	AAT		300
Lys	Pro	Phe	His	Leu	Asn	Tyr	His	Val	Asp	His	Leu	Asp	Ser	Ser	Asn		
				65					70						75		
AGT	TTT	TCC	GTG	ACA	AAT	GCT	TTC	TGC	TCC	CAG	TTC	TCG	AGA	GGG	GTG		348
Ser	Phe	Ser	Val	Thr	Asn	Ala	Phe	Cys	Ser	Gln	Phe	Ser	Arg	Gly	Val		
			80					85					90				
TAT	GCC	ATC	TTT	GGA	TTC	TAT	GAC	CAG	ATG	TCA	ATG	AAC	ACC	CTG	ACC		396
Tyr	Ala	Ile	Phe	Gly	Phe	Tyr	Asp	Gln	Met	Ser	Met	Asn	Thr	Leu	Thr		
		95					100					105					
TCC	TTC	TGT	GGG	GCC	CTG	CAC	ACA	TCC	TTT	GTT	ACG	CCT	AGC	TTC	CCC		444
Ser	Phe	Cys	Gly	Ala	Leu	His	Thr	Ser	Phe	Val	Thr	Pro	Ser	Phe	Pro		
	110						115					120					
ACT	GAC	GCA	GAT	GTG	CAG	TTT	GTC	ATC	CAG	ATG	CGC	CCA	GCC	TTG	AAG		492
Thr	Asp	Ala	Asp	Val	Gln	Phe	Val	Ile	Gln	Met	Arg	Pro	Ala	Leu	Lys		
	125				130					135					140		
GGC	GCT	ATT	CTG	AGT	CTT	CTG	GGT	CAT	TAC	AAG	IGG	GAG	AAG	TTT	GTG		540
Gly	Ala	Ile	Leu	Ser	Leu	Leu	Gly	His	Tyr	Lys	Trp	Glu	Lys	Phe	Val		
				145					150						155		

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TAC	CTC	TAT	GAC	ACA	GAA	CGA	GGA	TTT	TCC	ATC	CTC	CAA	GCG	ATT	ATG	588
Tyr	Leu	Tyr	Asp	Thr	Glu	Arg	Gly	Phe	Ser	Ile	Leu	Gln	Ala	Ile	Met	
			160					165					170			
GAA	GCA	GCA	GTG	CAA	AAC	AAC	TGG	CAA	GTA	ACA	GCA	AGG	TCT	GTG	GGA	636
Glu	Ala	Ala	Val	Gln	Asn	Asn	Trp	Gln	Val	Thr	Ala	Arg	Ser	Val	Gly	
			175				180					185				
AAC	ATA	AAG	GAC	GTC	CAA	GAA	TTC	AGG	CGC	ATC	ATT	GAA	GAA	ATG	GAC	684
Asn	Ile	Lys	Asp	Val	Gln	Glu	Phe	Arg	Arg	Ile	Ile	Glu	Glu	Met	Asp	
	190					195					200					
AGG	AGG	CAG	GAA	AAG	CGA	TAC	TTG	ATT	GAC	TGC	GAA	GTC	GAA	AGG	ATT	732
Arg	Arg	Gln	Glu	Lys	Arg	Tyr	Leu	Ile	Asp	Cys	Glu	Val	Glu	Arg	Ile	
205					210					215					220	
AAC	ACA	ATT	TTG	GAA	CAG	GTT	GTG	ATC	CTA	GGG	AAA	CAC	TCA	AGA	GGT	780
Asn	Thr	Ile	Leu	Glu	Gln	Val	Val	Ile	Leu	Gly	Lys	His	Ser	Arg	Gly	
				225					230					235		
TAT	CAC	TAC	ATG	CTC	GCT	AAC	CTG	GGT	TTT	ACT	GAT	ATT	TTA	CTG	GAA	828
Tyr	His	Tyr	Met	Leu	Ala	Asn	Leu	Gly	Phe	Thr	Asp	Ile	Leu	Leu	Glu	
			240					245					250			
AGA	GTC	ATG	CAT	GGG	GGA	GCC	AAC	ATT	ACA	GGT	TTC	CAG	ATT	GTC	AAC	876
Arg	Val	Met	His	Gly	Gly	Ala	Asn	Ile	Thr	Gly	Phe	Gln	Ile	Val	Asn	
		255					260					265				
AAT	GAA	AAC	CCT	ATG	GTT	CAG	CAG	TTC	ATA	CAG	CGC	TGG	GTG	AGG	CTG	924
Asn	Glu	Asn	Pro	Met	Val	Gln	Gln	Phe	Ile	Gln	Arg	Trp	Val	Arg	Leu	
	270					275					280					
GAT	GAA	AGG	GAA	TTC	CCT	GAA	GCC	AAG	AAT	GCA	CCA	CTA	AAG	TAT	ACA	972
Asp	Glu	Arg	Glu	Phe	Pro	Glu	Ala	Lys	Asn	Ala	Pro	Leu	Lys	Tyr	Thr	
285					290					295					300	
TCT	GCA	TTG	ACA	CAC	GAC	GCA	ATA	CTG	GTC	ATA	GCA	GAA	GCT	TTC	CGC	1020
Ser	Ala	Leu	Thr	His	Asp	Ala	Ile	Leu	Val	Ile	Ala	Glu	Ala	Phe	Arg	
				305					310					315		
TAC	CTG	AGG	AGG	CAG	CGA	GTA	GAT	GTG	TCC	CGG	AGA	GGA	AGT	GCT	GGA	1068
Tyr	Leu	Arg	Arg	Gln	Arg	Val	Asp	Val	Ser	Arg	Arg	Gly	Ser	Ala	Gly	
			320					325					330			
GAC	TGC	TTA	GCA	AAT	CCT	GCT	GTG	CCC	TGG	AGT	CAA	GGA	ATT	GAT	ATT	1116
Asp	Cys	Leu	Ala	Asn	Pro	Ala	Val	Pro	Trp	Ser	Gln	Gly	Ile	Asp	Ile	
		335					340					345				
GAG	AGA	GCT	CTG	AAA	ATG	GTG	CAA	GTA	CAA	GGA	ATG	ACT	GGA	AAT	ATT	1164
Glu	Arg	Ala	Leu	Lys	Met	Val	Gln	Val	Gln	Gly	Met	Thr	Gly	Asn	Ile	
	350					355					360					
CAA	TTT	GAC	ACT	TAT	GGA	CGT	AGG	ACA	AAT	TAT	ACC	ATC	GAT	GTG	TAT	1212
Gln	Phe	Asp	Thr	Tyr	Gly	Arg	Arg	Thr	Asn	Tyr	Thr	Ile	Asp	Val	Tyr	
					370					375					380	
GAA	ATG	AAA	GTC	AGT	GGC	TCT	CGA	AAA	GCT	GGC	TAC	TGG	AAC	GAG	TAT	1260
Glu	Met	Lys	Val	Ser	Gly	Ser	Arg	Lys	Ala	Gly	Tyr	Trp	Asn	Glu	Tyr	
				385					390					395		
GAA	AGG	TTT	GTG	CCT	TTC	TCA	GAT	CAG	CAA	ATC	AGC	AAT	GAC	AGT	GCA	1308
Glu	Arg	Phe	Val	Pro	Phe	Ser	Asp	Gln	Gln	Ile	Ser	Asn	Asp	Ser	Ala	
			400					405					410			
TCC	TCA	GAG	AAT	CGG	ACC	ATA	GTA	GTG	ACT	ACC	ATT	CTG	GAA	TCA	CCA	1356
Ser	Ser	Glu	Asn	Arg	Thr	Ile	Val	Val	Thr	Thr	Ile	Leu	Glu	Ser	Pro	
		415					420					425				
TAT	GTA	ATG	TAC	AAG	AAG	AAC	CAT	GAG	CAA	CTG	GAA	GGA	AAT	GAA	CGA	1404
Tyr	Val	Met	Tyr	Lys	Lys	Asn	His	Glu	Gln	Leu	Glu	Gly	Asn	Glu	Arg	
	430					435					440					
TAT	GAA	GGC	TAT	TGT	GTA	GAC	CTA	GCC	TAT	GAA	ATA	GCC	AAA	CAT	GTA	1452
Tyr	Glu	Gly	Tyr	Cys	Val	Asp	Leu	Ala	Tyr	Glu	Ile	Ala	Lys	His	Val	
				450						455					460	
AGG	ATC	AAA	TAC	AAA	TTG	TCC	ATC	GTT	GGT	GAC	GGG	AAA	TAT	GGT	GCA	1500
Arg	Ile	Lys	Tyr	Lys	Leu	Ser	Ile	Val	Gly	Asp	Gly	Lys	Tyr	Gly	Ala	
				465					470					475		

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AGG Arg	GAT Asp	CCA Pro	GAG Glu 480	ACT Thr	AAA Lys	ATA Ile	TGG Trp	AAC Asn 485	GGC Gly	ATG Met	GTT Val	GGG Gly 490	GAA Glu 490	CTT Leu	GTC Val	1548
TAT Tyr	GGG Gly 495	AGA Arg	GCT Ala	GAT Asp	ATA Ile	GCT Ala	GTT Val 500	GCT Ala	CCA Pro	CTC Leu	ACT Thr	ATA Ile 505	ACA Thr	TTG Leu	GTC Val	1596
CGT Arg 510	GAA Glu	GAA Glu	GTC Val	ATA Ile	GAT Asp	TTT Phe 515	TCA Ser	AAG Lys	CCA Pro	TTC Phe	ATG Met 520	AGC Ser	CTG Leu	GGC Gly	ATC Ile	1644
TCC Ser 525	ATC Ile	ATG Met	ATA Ile	AAG Lys	AAG Lys 530	CCT Pro	CAG Gln	AAA Lys	TCA Ser	AAA Lys 535	CCA Pro	GGC Gly	GTA Val	TTC Phe	TCA Ser 540	1692
TTT Phe	CTG Leu	GAT Asp	CCC Pro	CTG Leu 545	GCT Ala	TAT Tyr	GAA Glu 550	ATC Ile	TGG Trp 550	ATG Met	TGC Cys	ATT Ile	GTC Val	TTT Phe 555	GCT Ala	1740
TAC Tyr	ATT Ile	GGA Gly	GTC Val 560	AGC Ser	GTA Val	GTT Val	CTT Leu	TTC Phe 565	CTA Leu	GTC Val	AGC Ser	AGG Arg 570	TTC Phe	AGT Ser	CCT Pro	1788
TAT Tyr	GAA Glu 575	TGG Trp	CAC His	TTG Leu	GAA Glu	GAC Asp	AAC Asn 580	AAT Asn	GAA Glu	GAA Glu	CCT Pro	CGT Arg 585	GAC Asp	CCA Pro	CAA Gln	1836
AGT Ser 590	CCT Pro	CCT Pro	GAT Asp	CCT Pro	CCA Pro	AAT Asn 595	GAA Glu	TTT Phe	GGA Gly	ATA Ile	TTT Phe 600	AAC Asn	AGT Ser	CTT Leu	TGG Trp	1884
TTT Phe 605	TCC Ser	TTG Leu	GGT Gly	GCC Ala	TTT Phe 610	ATG Met	CAG Gln	CAA Gln	GGA Gly	TGT Cys 615	GAT Asp	ATT Ile	TCT Ser	CCA Pro	AGA Arg 620	1932
TCA Ser	CTC Leu	TCC Ser	GGG Gly	CGC Arg 625	ATT Ile	GTT Val	GGA Gly	GGG Gly	GTT Val 630	TGG Trp	TGG Trp	TTC Phe	TTC Phe	ACC Thr 635	CTG Leu	1980
ATC Ile	ATA Ile	ATT Ile	TCT Ser 640	TCC Ser	TAT Tyr	ACT Thr	GCC Ala	AAT Asn 645	CTC Leu	GCT Ala	GCT Ala	TTC Phe 650	CTG Leu	ACT Thr	GTG Val	2028
GAG Glu	AGG Arg 655	ATG Met	GTT Val	TCT Ser	CCC Pro	ATA Ile	GAG Glu 660	AGT Ser	GCT Ala	GAA Glu	GAC Asp	TTA Leu 665	GCT Ala	AAA Lys	CAG Gln	2076
ACT Thr	GAA Glu 670	ATT Ile	GCA Ala	TAT Tyr	GGG Gly	ACC Thr 675	CTG Leu	GAC Asp	TCC Ser	GGT Gly	TCA Ser 680	ACA Thr	AAA Lys	GAA Glu	TTT Phe	2124
TTC Phe 685	AGA Arg	AGA Arg	TCC Ser	AAA Lys	ATT Ile 690	GCT Ala	GTG Val	TAC Tyr	GAG Glu	AAA Lys 695	ATG Met	TGG Trp	TCT Ser	TAC Tyr	ATG Met 700	2172
AAA Lys	TCA Ser	GCG Ala	GAG Glu	CCA Pro 705	TCT Ser	GTG Val	TTT Phe	ACC Thr 710	AAA Lys	ACA Thr	ACA Thr	GCA Ala	GAC Asp	GGA Gly 715	GTG Val	2220
GCC Ala	CGA Arg	GTG Val	CGA Arg 720	AAG Lys	TCC Ser	AAG Lys	GGA Gly	AAG Lys 725	TTC Phe	GCC Ala	TTC Phe	CTG Leu	CTG Leu	GAG Glu	TCA Ser	2268
ACC Thr	ATG Met	AAT Asn 735	GAG Glu	TAC Tyr	ATT Ile	GAG Glu 740	CAG Gln	AGA Arg	AAA Lys	CCA Pro	TGT Cys	GAT Asp 745	ACG Thr	ATG Met	AAA Lys	2316
GTT Val 750	GGT Gly	GGA Gly	AAT Asn	CTG Leu	GAT Asp	TCC Ser 755	AAA Lys	GGC Gly	TAT Tyr	GGT Gly	GTG Val 760	GCA Ala	ACC Thr	CCT Pro	AAA Lys	2364
GGC Gly 765	TCA Ser	GCA Ala	TTA Leu	GGA Gly	AAT Asn 770	GCT Ala	GTT Val	AAC Asn	CTG Leu	GCA Ala 775	GTA Val	TTA Leu	AAA Lys	CTG Leu	AAT Asn 780	2412
GAG Glu	CAA Gln	GGC Gly	CTC Leu	TTG Leu 785	GAC Asp	AAA Lys	TTG Leu	AAA Lys	AAC Asn 790	AAA Lys	TGG Trp	TGG Trp	TAC Tyr	GAC Asp	AAA Lys 795	2460

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GGA	GAG	TGC	GGC	AGC	GGG	GGC	GGT	GAC	TCC	AAG	GAC	AAG	ACC	AGC	GCT	2508
Gly	Glu	Cys	Gly	Ser	Gly	Gly	Gly	Asp	Ser	Lys	Asp	Lys	Thr	Ser	Ala	
			800					805					810			
CTG	AGC	CTG	AGC	AAT	GTG	GCA	GGC	GTT	TTC	TAT	ATA	CTT	GTC	GGA	GGT	2556
Leu	Ser	Leu	Ser	Asn	Val	Ala	Gly	Val	Phe	Tyr	Ile	Leu	Val	Gly	Gly	
			815				820					825				
CTG	GGG	CTG	GCC	ATG	ATG	GTG	GCT	TTG	ATA	GAA	TTC	TGT	TAC	AAA	TCA	2604
Leu	Gly	Leu	Ala	Met	Met	Val	Ala	Leu	Ile	Glu	Phe	Cys	Tyr	Lys	Ser	
	830					835					840					
CGG	GCA	GAG	TCC	AAA	CGC	ATG	AAA	CTC	ACA	AAG	AAC	ACC	CAA	AAC	TTT	2652
Arg	Ala	Glu	Ser	Lys	Arg	Met	Lys	Leu	Thr	Lys	Asn	Thr	Gln	Asn	Phe	
	845				850					855					860	
AAG	CCT	GCT	CCT	GCC	ACC	AAC	ACT	CAG	AAT	TAT	GCT	ACA	TAC	AGA	GAA	2700
Lys	Pro	Ala	Pro	Ala	Thr	Asn	Thr	Gln	Asn	Tyr	Ala	Thr	Tyr	Arg	Glu	
				865					870					875		
GGC	TAC	AAC	GTG	TAT	GGA	ACA	GAG	AGT	GTT	AAG	ATC	TAGGGATCCC				2746
Gly	Tyr	Asn	Val	Tyr	Gly	Thr	Glu	Ser	Val	Lys	Ile					
			880					885								
TCCCCACTGG AGGCATGTGA TGAGAGGAAA TCACCGAAAA CGTGGCTGCT TCAAGGATCC																2806
TGAGCCAGAT TTCACTCTCC TTGGTGTCCG GCATGACACG AATATTGCTG ATGGTGCAAT																2866
GACCTTTCAA TAGGAAAAAC TGGTTTTTTT TTCCTTCAGT GCCTTATGGA ACACTCTGAG																2926
ACTCGCGACA ATGCAAACCA TCATTGAAAT CTTTTTGCTT TGCTTGAAAA AAAAAAAAAA																2986
AAA																2989

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Gly	Gln	Ser	Val	Leu	Arg	Ala	Val	Phe	Phe	Leu	Val	Leu	Gly	Leu	
1				5					10					15		
Leu	Gly	His	Ser	His	Gly	Gly	Phe	Pro	Asn	Thr	Ile	Ser	Ile	Gly	Gly	
			20					25					30			
Leu	Phe	Met	Arg	Asn	Thr	Val	Gln	Glu	His	Ser	Ala	Phe	Arg	Phe	Ala	
		35					40					45				
Val	Gln	Leu	Tyr	Asn	Thr	Asn	Gln	Asn	Thr	Thr	Glu	Lys	Pro	Phe	His	
	50					55					60					
Leu	Asn	Tyr	His	Val	Asp	His	Leu	Asp	Ser	Ser	Asn	Ser	Phe	Ser	Val	
	65				70					75					80	
Thr	Asn	Ala	Phe	Cys	Ser	Gln	Phe	Ser	Arg	Gly	Val	Tyr	Ala	Ile	Phe	
				85					90					95		
Gly	Phe	Tyr	Asp	Gln	Met	Ser	Met	Asn	Thr	Leu	Thr	Ser	Phe	Cys	Gly	
			100					105					110			
Ala	Leu	His	Thr	Ser	Phe	Val	Thr	Pro	Ser	Phe	Pro	Thr	Asp	Ala	Asp	
		115					120					125				
Val	Gln	Phe	Val	Ile	Gln	Met	Arg	Pro	Ala	Leu	Lys	Gly	Ala	Ile	Leu	
	130					135					140					
Ser	Leu	Leu	Gly	His	Tyr	Lys	Trp	Glu	Lys	Phe	Val	Tyr	Leu	Tyr	Asp	
	145				150					155					160	
Thr	Glu	Arg	Gly	Phe	Ser	Ile	Leu	Gln	Ala	Ile	Met	Glu	Ala	Ala	Val	
				165					170					175		

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Gln	Asn	Asn	Trp 180	Gln	Val	Thr	Ala	Arg 185	Ser	Val	Gly	Asn	Ile 190	Lys	Asp
Val	Gln	Glu 195	Phe	Arg	Arg	Ile	Ile 200	Glu	Glu	Met	Asp	Arg 205	Arg	Gln	Glu
Lys	Arg 210	Tyr	Leu	Ile	Asp	Cys 215	Glu	Val	Glu	Arg	Ile 220	Asn	Thr	Ile	Leu
Glu 225	Gln	Val	Val	Ile	Leu 230	Gly	Lys	His	Ser	Arg 235	Gly	Tyr	His	Tyr	Met 240
Leu	Ala	Asn	Leu	Gly 245	Phe	Thr	Asp	Ile	Leu 250	Leu	Glu	Arg	Val	Met 255	His
Gly	Gly	Ala	Asn 260	Ile	Thr	Gly	Phe	Gln 265	Ile	Val	Asn	Asn	Glu 270	Asn	Pro
Met	Val	Gln 275	Gln	Phe	Ile	Gln	Arg 280	Trp	Val	Arg	Leu	Asp 285	Glu	Arg	Glu
Phe	Pro 290	Glu	Ala	Lys	Asn	Ala 295	Pro	Leu	Lys	Tyr	Thr 300	Ser	Ala	Leu	Thr
His 305	Asp	Ala	Ile	Leu	Val 310	Ile	Ala	Glu	Ala	Phe 315	Arg	Tyr	Leu	Arg	Arg 320
Gln	Arg	Val	Asp 325	Val	Ser	Arg	Arg	Gly	Ser 330	Ala	Gly	Asp	Cys	Leu 335	Ala
Asn	Pro	Ala	Val 340	Pro	Trp	Ser	Gln	Gly 345	Ile	Asp	Ile	Glu	Arg 350	Ala	Leu
Lys	Met 355	Val	Gln	Val	Gln	Gly	Met 360	Thr	Gly	Asn	Ile	Gln 365	Phe	Asp	Thr
Tyr 370	Gly	Arg	Arg	Thr	Asn	Tyr 375	Thr	Ile	Asp	Val	Tyr 380	Glu	Met	Lys	Val
Ser 385	Gly	Ser	Arg	Lys	Ala 390	Gly	Tyr	Trp	Asn	Glu 395	Tyr	Glu	Arg	Phe	Val 400
Pro	Phe	Ser	Asp 405	Gln	Gln	Ile	Ser	Asn 410	Asp	Ser	Ala	Ser	Ser	Glu 415	Asn
Arg	Thr	Ile	Val 420	Val	Thr	Thr	Ile	Leu 425	Glu	Ser	Pro	Tyr	Val 430	Met	Tyr
Lys	Lys	Asn 435	His	Glu	Gln	Leu	Glu 440	Gly	Asn	Glu	Arg	Tyr 445	Glu	Gly	Tyr
Cys	Val 450	Asp	Leu	Ala	Tyr	Glu 455	Ile	Ala	Lys	His 460	Val	Arg	Ile	Lys	Tyr
Lys 465	Leu	Ser	Ile	Val	Gly 470	Asp	Gly	Lys	Tyr	Gly 475	Ala	Arg	Asp	Pro	Glu 480
Thr	Lys	Ile	Trp 485	Asn	Gly	Met	Val	Gly 490	Glu	Leu	Val	Tyr	Gly	Arg 495	Ala
Asp	Ile	Ala	Val 500	Ala	Pro	Leu	Thr	Ile 505	Thr	Leu	Val	Arg	Glu 510	Glu	Val
Ile	Asp	Phe 515	Ser	Lys	Pro	Phe	Met 520	Ser	Leu	Gly	Ile	Ser 525	Ile	Met	Ile
Lys 530	Lys	Pro	Gln	Lys	Ser	Lys 535	Pro	Gly	Val	Phe	Ser 540	Phe	Leu	Asp	Pro
Leu 545	Ala	Tyr	Glu	Ile	Trp 550	Met	Cys	Ile	Val	Phe 555	Ala	Tyr	Ile	Gly	Val 560
Ser	Val	Val	Leu	Phe 565	Leu	Val	Ser	Arg	Phe 570	Ser	Pro	Tyr	Glu	Trp 575	His
Leu	Glu	Asp	Asn 580	Asn	Glu	Glu	Pro	Arg 585	Asp	Pro	Gln	Ser	Pro 590	Pro	Asp
Pro	Pro	Asn 595	Glu	Phe	Gly	Ile	Phe 600	Asn	Ser	Leu	Trp	Phe 605	Ser	Leu	Gly

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Ala	Phe	Met	Gln	Gln	Gly	Cys	Asp	Ile	Ser	Pro	Arg	Ser	Leu	Ser	Gly
	610					615					620				
Arg	Ile	Val	Gly	Gly	Val	Trp	Trp	Phe	Phe	Thr	Leu	Ile	Ile	Ile	Ser
625					630					635					640
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Thr	Val	Glu	Arg	Met	Val
				645					650					655	
Ser	Pro	Ile	Glu	Ser	Ala	Glu	Asp	Leu	Ala	Lys	Gln	Thr	Glu	Ile	Ala
			660					665					670		
Tyr	Gly	Thr	Leu	Asp	Ser	Gly	Ser	Thr	Lys	Glu	Phe	Phe	Arg	Arg	Ser
		675					680					685			
Lys	Ile	Ala	Val	Tyr	Glu	Lys	Met	Trp	Ser	Tyr	Met	Lys	Ser	Ala	Glu
	690					695					700				
Pro	Ser	Val	Phe	Thr	Lys	Thr	Thr	Ala	Asp	Gly	Val	Ala	Arg	Val	Arg
705					710					715					720
Lys	Ser	Lys	Gly	Lys	Phe	Ala	Phe	Leu	Leu	Glu	Ser	Thr	Met	Asn	Glu
				725				730						735	
Tyr	Ile	Glu	Gln	Arg	Lys	Pro	Cys	Asp	Thr	Met	Lys	Val	Gly	Gly	Asn
			740					745					750		
Leu	Asp	Ser	Lys	Gly	Tyr	Gly	Val	Ala	Thr	Pro	Lys	Gly	Ser	Ala	Leu
		755					760					765			
Gly	Asn	Ala	Val	Asn	Leu	Ala	Val	Leu	Lys	Leu	Asn	Glu	Gln	Gly	Leu
	770					775					780				
Leu	Asp	Lys	Leu	Lys	Asn	Lys	Trp	Trp	Tyr	Asp	Lys	Gly	Glu	Cys	Gly
785					790					795					800
Ser	Gly	Gly	Gly	Asp	Ser	Lys	Asp	Lys	Thr	Ser	Ala	Leu	Ser	Leu	Ser
				805					810					815	
Asn	Val	Ala	Gly	Val	Phe	Tyr	Ile	Leu	Val	Gly	Gly	Leu	Gly	Leu	Ala
			820					825					830		
Met	Met	Val	Ala	Leu	Ile	Glu	Phe	Cys	Tyr	Lys	Ser	Arg	Ala	Glu	Ser
		835					840					845			
Lys	Arg	Met	Lys	Leu	Thr	Lys	Asn	Thr	Gln	Asn	Phe	Lys	Pro	Ala	Pro
	850					855					860				
Ala	Thr	Asn	Thr	Gln	Asn	Tyr	Ala	Thr	Tyr	Arg	Glu	Gly	Tyr	Asn	Val
865					870					875					880
Tyr	Gly	Thr	Glu	Ser	Val	Lys	Ile								
				885											

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA to mRNA

(v i) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) DEVELOPMENTAL STAGE: adult
- (C) TISSUE TYPE: brain

(i x) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 317..1191

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CGGGTCCTGA	CAGCCCCTTG	GCCTCCCAGC	ATGGGGAAGC	GTGAGGAGTT	GCCCAGCAGT	60
GAGCAGCCCC	CCTCACTCCT	GGCCCCATGA	GCCGCAGCCA	CAGGCAGCAG	AGGAGGGCTA	120

-continued

Gln Arg Glu Tyr Pro Gly Ser Glu
285 290

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: protein

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Arg	Ile	Ile	Ser	Arg	Gln	Ile	Val	Leu	Leu	Phe	Ser	Gly	Phe	Trp
1				5					10					15	
Gly	Leu	Ala	Met	Gly	Ala	Phe	Pro	Ser	Ser	Val	Gln	Ile	Gly	Gly	Leu
			20					25					30		
Phe	Ile	Arg	Asn	Thr	Asp	Gln	Glu	Tyr	Thr	Ala	Phe	Arg	Leu	Ala	Ile
		35					40					45			
Phe	Leu	His	Asn	Thr	Ser	Pro	Asn	Ala	Ser	Glu	Ala	Pro	Phe	Asn	Leu
	50					55					60				
Val	Pro	His	Val	Asp	Asn	Ile	Glu	Thr	Ala	Asn	Ser	Phe	Ala	Val	Thr
65					70					75					80
Asn	Ala	Phe	Cys	Ser	Gln	Tyr	Ser	Arg	Gly	Val	Phe	Ala	Ile	Phe	Gly
				85					90					95	
Leu	Tyr	Asp	Lys	Arg	Ser	Val	His	Thr	Leu	Thr	Ser	Phe	Cys	Ser	Ala
			100					105					110		
Leu	His	Ile	Ser	Leu	Ile	Thr	Pro	Ser	Phe	Pro	Thr	Glu	Gly	Glu	Ser
		115					120					125			
Gln	Phe	Val	Leu	Gln	Leu	Arg	Pro	Ser	Leu	Arg	Gly	Ala	Leu	Leu	Ser
	130					135					140				
Leu	Leu	Asp	His	Tyr	Glu	Trp	Asn	Cys	Phe	Val	Phe	Leu	Tyr	Asp	Thr
145					150					155					160
Asp	Arg	Gly	Tyr	Ser	Ile	Leu	Gln	Ala	Ile	Leu	Glu	Lys	Ala	Gly	Gln
				165					170					175	
Asn	Gly	Trp	His	Val	Ser	Ala	Ile	Cys	Val	Glu	Asn	Phe	Asn	Asp	Val
			180					185					190		
Ser	Tyr	Arg	Gln	Leu	Leu	Glu	Glu	Leu	Asp	Arg	Arg	Gln	Glu	Lys	Lys
		195					200					205			
Phe	Val	Ile	Asp	Cys	Glu	Ile	Glu	Arg	Leu	Gln	Asn	Ile	Leu	Glu	Gln
	210					215					220				
Ile	Val	Ser	Val	Gly	Lys	His	Val	Lys	Gly	Tyr	His	Tyr	Ile	Ile	Ala
225					230					235					240
Asn	Leu	Gly	Phe	Lys	Asp	Ile	Ser	Leu	Glu	Arg	Phe	Ile	His	Gly	Gly
				245					250					255	
Ala	Asn	Val	Thr	Gly	Phe	Gln	Leu	Val	Asp	Phe	Asn	Thr	Pro	Met	Val
			260					265					270		
Ile	Lys	Leu	Met	Asp	Arg	Trp	Lys	Lys	Leu	Asp	Gln	Arg	Glu	Tyr	Pro
		275					280					285			
Gly	Ser	Glu													
		290													

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

-continued

(i i) MOLECULE TYPE: cDNA to mRNA

(v i) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(B) DEVELOPMENTAL STAGE: adult
(C) TISSUE TYPE: brain

(i x) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 317..1191

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGGGTCCTGA	CAGCCCCTTG	GCCTCCCAGC	ATGGGGAAGC	GTGAGGAGTT	GCCCAGCAGT												60
GAGCAGCCCC	CCTCACTCCT	GGCCCCATGA	GCCGCAGCCA	CAGGCAGCAG	AGGAGGGCTA												120
AGGAGAACTA	GTCATAATCT	TAAACCACCG	AAACCTCTTT	CCTTTTTTTT	CTTTCTTTTC												180
TTTCTTTTCT	TTTTTTTTTT	TTTTTTTGG	TTGATTTTAA	TTTTAGCGCC	ATCGTCTTCA												240
ATGCTTCTCT	GAACAGCCTT	TAGGAAGAGT	GCGAGAGAAA	GAGAGAGAGC	GCGCGCCAGG												300
GAGAGGAGAA	AAGAAG	ATG	AGG	ATT	ATT	TCC	AGA	CAG	ATT	GTC	TTG	TTA					349
		Met	Arg	Ile	Ile	Ser	Arg	Gln	Ile	Val	Leu	Leu					
		1				5					10						
TTT	TCT	GGA	TTT	TGG	GGA	CTC	GCC	ATG	GGA	GCC	TTT	CCG	AGC	AGC	GTG		397
Phe	Ser	Gly	Phe	Trp	Gly	Leu	Ala	Met	Gly	Ala	Phe	Pro	Ser	Ser	Val		
			15					20					25				
CAA	ATA	GGT	GGT	CTC	TTC	ATC	CGA	AAC	ACA	GAT	CAG	GAA	TAC	ACT	GCT		445
Gln	Ile	Gly	Gly	Leu	Phe	Ile	Arg	Asn	Thr	Asp	Gln	Glu	Tyr	Thr	Ala		
			30				35					40					
TTT	CGA	TTA	GCA	ATT	TTT	CTT	CAT	AAC	ACC	AGC	CCC	AAT	GCG	TCG	GAA		493
Phe	Arg	Leu	Ala	Ile	Phe	Leu	His	Asn	Thr	Ser	Pro	Asn	Ala	Ser	Glu		
	45					50					55						
GCT	CCT	TTT	AAT	TTG	GTA	CCT	CAT	GTG	GAC	AAC	ATT	GAG	ACA	GCC	AAC		541
Ala	Pro	Phe	Asn	Leu	Val	Pro	His	Val	Asp	Asn	Ile	Glu	Thr	Ala	Asn		
	60				65				70						75		
AGT	TTT	GCT	GTA	ACA	AAC	GCC	TTC	TGT	TCC	CAG	TAT	TCT	AGA	GGA	GTA		589
Ser	Phe	Ala	Val	Thr	Asn	Ala	Phe	Cys	Ser	Gln	Tyr	Ser	Arg	Gly	Val		
				80				85						90			
TTT	GCC	ATT	TTT	GGA	CTC	TAT	GAT	AAG	AGG	TCG	GTA	CAT	ACC	TTG	ACC		637
Phe	Ala	Ile	Phe	Gly	Leu	Tyr	Asp	Lys	Arg	Ser	Val	His	Thr	Leu	Thr		
			95					100					105				
TCA	TTC	TGC	AGC	GCC	TTA	CAT	ATC	TCC	CTC	ATC	ACA	CCA	AGT	TTC	CCT		685
Ser	Phe	Cys	Ser	Ala	Leu	His	Ile	Ser	Leu	Ile	Thr	Pro	Ser	Phe	Pro		
		110					115					120					
ACT	GAG	GGG	GAG	AGC	CAG	TTT	GTG	CTG	CAA	CTA	AGA	CCT	TCG	TTA	CGA		733
Thr	Glu	Gly	Glu	Ser	Gln	Phe	Val	Leu	Gln	Leu	Arg	Pro	Ser	Leu	Arg		
	125					130					135						
GGA	GCA	CTC	TTG	AGT	TTG	CTG	GAT	CAC	TAC	GAA	IGG	AAC	TGT	TTT	GTC		781
Gly	Ala	Leu	Leu	Ser	Leu	Leu	Asp	His	Tyr	Glu	Trp	Asn	Cys	Phe	Val		
	140				145					150					155		
TTC	CTG	TAT	GAC	ACA	GAC	AGG	GGA	TAC	TCG	ATA	CTC	CAA	GCT	ATT	TTG		829
Phe	Leu	Tyr	Asp	Thr	Asp	Arg	Gly	Tyr	Ser	Ile	Leu	Gln	Ala	Ile	Leu		
				160					165					170			
GAA	AAA	GCA	GGA	CAA	AAT	GGT	TGG	CAT	GTC	AGC	GCT	ATA	TGT	GTG	GAA		877
Glu	Lys	Ala	Gly	Gln	Asn	Gly	Trp	His	Val	Ser	Ala	Ile	Cys	Val	Glu		
			175				180						185				
AAT	TTT	AAT	GAT	GTC	AGC	TAT	AGG	CAA	CTT	CTA	GAA	GAA	CTT	GAC	AGA		925
Asn	Phe	Asn	Asp	Val	Ser	Tyr	Arg	Gln	Leu	Leu	Glu	Glu	Leu	Asp	Arg		
		190					195					200					
AGA	CAA	GAG	AAG	AAG	TTT	GTA	ATA	GAC	IGT	GAG	ATA	GAG	AGA	CTT	CAA		973
Arg	Gln	Glu	Lys	Lys	Phe	Val	Ile	Asp	Cys	Glu	Ile	Glu	Arg	Leu	Gln		
	205					210						215					

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AAC Asn 220	ATA Ile	TTA Leu	GAA Glu	CAG Gln	ATT Ile 225	GTA Val	AGT Ser	GTT Val	GGA Gly	AAG Lys 230	CAT His	GTT Val	AAA Lys	GGC Gly	TAC Tyr 235	1021
CAT His	TAT Tyr	ATC Ile	ATT Ile	GCA Ala 240	AAC Asn	TTG Leu	GGA Gly	TTC Phe	AAG Lys 245	GAT Asp	ATT Ile	TCT Ser	CTT Leu	GAG Glu 250	AGG Arg	1069
TTT Phe	ATA Ile	CAT His	GGT Gly 255	GGA Gly	GCC Ala	AAT Asn	GTT Val 260	ACT Thr	GGA Gly	TTC Phe	CAG Gln	TTG Leu	GTG Val 265	GAT Asp	TTT Phe	1117
AAT Asn	ACA Thr	CCT Pro 270	ATG Met	GTA Val	ATC Ile	AAA Lys 275	CTA Leu	ATG Met	GAT Asp	CGC Arg	TGG Trp	AAG Lys 280	AAA Lys	CTA Leu	GAT Asp	1165
CAG Gln 285	AGA Arg	GAG Glu	TAT Tyr	CCA Pro	GGA Gly	TCT Ser 290	GAG Glu	CC								1191

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: protein

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met 1	Arg	Ile	Ile	Ser 5	Arg	Gln	Ile	Val	Leu 10	Leu	Phe	Ser	Gly	Phe 15	Trp
Gly	Leu	Ala	Met 20	Gly	Ala	Phe	Pro	Ser 25	Ser	Val	Gln	Ile	Gly 30	Gly	Leu
Phe	Ile	Arg 35	Asn	Thr	Asp	Gln	Glu 40	Tyr	Thr	Ala	Phe	Arg 45	Leu	Ala	Ile
Phe 50	Leu	His	Asn	Thr	Ser	Pro 55	Asn	Ala	Ser	Glu	Ala 60	Pro	Phe	Asn	Leu
Val 65	Pro	His	Val	Asp	Asn 70	Ile	Glu	Thr	Ala	Asn 75	Ser	Phe	Ala	Val	Thr 80
Asn	Ala	Phe	Cys 85	Ser	Gln	Tyr	Ser	Arg	Gly 90	Val	Phe	Ala	Ile	Phe 95	Gly
Leu	Tyr	Asp 100	Lys	Arg	Ser	Val	His 105	Thr	Leu	Thr	Ser	Phe	Cys 110	Ser	Ala
Leu	His 115	Ile	Ser	Leu	Ile	Thr	Pro 120	Ser	Phe	Pro	Thr	Glu 125	Gly	Glu	Ser
Gln 130	Phe	Val	Leu	Gln	Leu	Arg 135	Pro	Ser	Leu	Arg	Gly 140	Ala	Leu	Leu	Ser
Leu 145	Leu	Asp	His	Tyr	Glu 150	Trp	Asn	Cys	Phe 155	Val	Phe	Leu	Tyr	Asp	Thr 160
Asp	Arg	Gly	Tyr 165	Ser	Ile	Leu	Gln	Ala	Ile 170	Leu	Glu	Lys	Ala	Gly 175	Gln
Asn	Gly	Trp 180	His	Val	Ser	Ala	Ile	Cys 185	Val	Glu	Asn	Phe	Asn 190	Asp	Val
Ser	Tyr	Arg 195	Gln	Leu	Leu	Glu	Glu 200	Leu	Asp	Arg	Arg	Gln 205	Glu	Lys	Lys
Phe 210	Val	Ile	Asp	Cys	Glu	Ile 215	Glu	Arg	Leu	Gln	Asn 220	Ile	Leu	Glu	Gln
Ile 225	Val	Ser	Val	Gly	Lys 230	His	Val	Lys	Gly	Tyr 235	His	Tyr	Ile	Ile	Ala 240
Asn	Leu	Gly	Phe 245	Lys	Asp	Ile	Ser	Leu	Glu	Arg 250	Phe	Ile	His	Gly 255	Gly

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Ala	Asn	Val	Thr	Gly	Phe	Gln	Leu	Val	Asp	Phe	Asn	Thr	Pro	Met	Val
			260					265					270		
Ile	Lys	Leu	Met	Asp	Arg	Trp	Lys	Lys	Leu	Asp	Gln	Arg	Glu	Tyr	Pro
		275					280					285			
Gly	Ser	Glu													
		290													

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATCTATGATT GGACCTGGGC

20

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ACATCTGCTC TTCATAGAC CAGC

24

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGC GATAAGC TTATGCAGCA CATTITGCC TTCTTCTGC

39

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGCCATTCC AGGCCTTCGT GTCA

24

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

-continued

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GATGGAAAAT ACGGAGCCCG A

2 1

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GCTGGGGAGC CGAGCCTGCT C

2 1

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TGACACGAAG GCCTGGAATG GCAT

2 4

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TGCGATGAAT TCTTACAATC CCGTGGCTCC CAAGGGCAT

3 9

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TACTTGGGTC TCTTCCAGTC CA

2 2

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: genomic DNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TGTGTGGTCT CGAGCATCAC TATT

2 4

We claim:

1. An isolated polynucleotide coding for a variant of a glutamate receptor subunit, the sequence of said polynucleotide being selected from the group consisting of:

- a) a polynucleotide comprising the nucleotide sequence shown in SEQ ID NO: 1 or SEQ ID NO: 3;
- b) a polynucleotide sequence coding for a protein comprising the amino acid sequence shown in SEQ ID NO: 2 or SEQ ID NO: 4; and
- c) a polynucleotide comprising a nucleotide sequence fully complementary to the nucleotide sequence of a) or b).

2. A method of preparing a glutamate receptor subunit, comprising the steps of

constructing a recombinant vector comprising the DNA sequence defined in claim 1 which codes for a glutamate receptor subunit;

transforming a compatible host with the recombinant vector such that the DNA sequence coding for the glutamate receptor subunit can be expressed by the host;

5 culturing the transformed host in a suitable growth medium to produce the glutamate receptor subunit; and recovering the glutamate receptor subunit from the medium.

3. The isolated polynucleotide of claim 1 wherein the polynucleotide comprises DNA.

10 4. The isolated polynucleotide of claim 1 wherein the polynucleotide comprises RNA.

5. A method for identifying functional ligands for glutamate receptors, which comprises transfecting cells with one or more DNA sequences coding for a glutamate receptor as claimed in claim 1, and detecting the effect on the signal transduction pathway caused in these cells by binding of the ligands to the receptor by a reporter system.

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